

SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

<120> PROTEIN HAVING PDZ DOMAIN SEQUENCE

<130> C2-905DP1PCT

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<150> JP 09-230356

JP 10-189944

<151> 1997-8-12

1998-6-19

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Gln Asn Val Ser Lys Glu Ser Phe Glu Arg Thr Ile Asn Ile Ala Lys			
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 Ala Pro Leu Cys Ser Val Pro Pro Pro Pro Pro Ser Ala Phe Ala Glu
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900

905

910

Ile Phe Ala Ser Asp Pro Ala Thr Cys Pro Ile Ile Pro Gly Cys Glu

915

920

925

930

Thr Thr Ile Glu Ile Ser Lys Gly Arg Thr Gly Leu Gly Leu Ser Ile

935

940

945

Val Gly Gly Ser Asp Thr Leu Leu Gly Ala Phe Ile Ile His Glu Val

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Tyr Glu Glu Gly Ala Ala Cys Lys Asp Gly Arg Leu Trp Ala Gly Asp

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Gln Ile Leu Glu Val Asn Gly Ile Asp Leu Arg Lys Ala Thr His Asp

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Glu Ala Ile Asn Val Leu Arg Gln Thr Pro Gln Arg Val Arg Leu Thr

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Gln His Leu Glu Leu Pro Lys Asp Gln Gly Gly Leu Gly Ile Ala Ile		
420	425	430
Ser Glu Glu Asp Thr Leu Ser Gly Val Ile Ile Lys Ser Leu Thr Glu		
435	440	445
His Gly Val Ala Ala Thr Asp Gly Arg Leu Lys Val Gly Asp Gln Ile		
450	455	460
Leu Ala Val Asp Asp Glu Ile Val Val Gly Tyr Pro Ile Glu Lys Phe		
465	470	475
Ile Ser Leu Leu Lys Thr Ala Lys Met Thr Val Lys Leu Thr Ile His		
485	490	495
Ala Glu Asn Pro Asp Ser Gln Ala Val Pro Ser Ala Ala Gly Ala Ala		
500	505	510

525

540

560

575

590

605

620

640

655

670

685

700

720

[illegible]

	725		730		735
Glu Val Gly Arg Ile Lys Ala Gly Pro Phe His Ser Glu Arg Arg Pro					
	740		745		750
Ser Gln Thr Ser Gln Val Ser Glu Gly Ser Leu Ser Ser Phe Thr Phe					
	755		760		765
Pro Leu Ser Gly Ser Ser Thr Ser Glu Ser Leu Glu Ser Ser Ser Lys					
	770		775		780
Lys Asn Ala Leu Ala Ser Glu Ile Gln Gly Leu Arg Thr Val Glu Met					
	785		790		795
Lys Lys Gly Pro Thr Asp Ser Leu Gly Ile Ser Ile Ala Gly Gly Val					
		805		810	815
Gly Ser Pro Leu Gly Asp Val Pro Ile Phe Ile Ala Met Met His Pro					
	820		825		830
Thr Gly Val Ala Ala Gln Thr Gln Lys Leu Arg Val Gly Asp Arg Ile					
	835		840		845
Val Thr Ile Cys Gly Thr Ser Thr Glu Gly Met Thr His Thr Gln Ala					
	850		855		860
Val Asn Leu Leu Lys Asn Ala Ser Gly Ser Ile Glu Met Gln Val Val					
	865		870		875
Ala Gly Gly Asp Val Ser Val Val Thr Gly His His Gln Glu Pro Ala					
	885		890		895
Ser Ser Ser Leu Ser Phe Thr Gly Leu Thr Ser Thr Ser Ile Phe Gln					
	900		905		910
Asp Asp Leu Gly Pro Pro Gln Cys Lys Ser Ile Thr Leu Glu Arg Gly					
	915		920		925
Pro Asp Gly Leu Gly Phe Ser Ile Val Gly Gly Tyr Gly Ser Pro His					
	930		935		940

Gly Asp Leu Pro Ile Tyr Val Lys Thr Val Phe Ala Lys Gly Ala Ala

945 950 955 960

Ser Glu Asp Gly Arg Leu Lys Arg Gly Asp Gln Ile Ile Ala Val Asn

965 970 975

Gly Gln Ser Leu Glu Gly Val Thr His Glu Glu Ala Val Ala Ile Leu

980 985 990

Lys Arg Thr Lys Gly Thr Val Thr Leu Met Val Leu Ser

995 1000 1005

<210> 3

<211> 4880

<212> DNA

<213> Homo sapience

<220>

<221> CDS

<222> (292)...(4410)

<400> 3

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ttggacacag cgggaagctc ttcagtggag acgagctatt ggaaaataag taacgcattc 120

agatgtttta aatcacagag aatacaaaga taaagaatgg aaaaggtct ccttcctgtc 180

ccaattcatc cagttctcat cacccttcat taggtaaatg gcataacttt acttggggaa 240

001120"0092560

1

15

30

50

65

80

95

110

130

145

160

175

190

Arg Ala Asp Leu Ala Leu Val Gly Thr Asn Asp Ala Asp Leu Val Asp

195	200	205	210	
gaa tcc aca ttt gag tct cca tac tct cct gaa aat gac agc atc tac				969
Glu Ser Thr Phe Glu Ser Pro Tyr Ser Pro Glu Asn Asp Ser Ile Tyr				
215	220	225		
tct act caa gcc tct att tta tct ctt cat ggc agt tct tgt ggt gat				1017
Ser Thr Gln Ala Ser Ile Leu Ser Leu His Gly Ser Ser Cys Gly Asp				
230	235	240		
ggc ctg aac tat ggt tct tcc ctt cca tca tct cct cct aag gat gtt				1065
Gly Leu Asn Tyr Gly Ser Ser Leu Pro Ser Ser Pro Pro Lys Asp Val				
245	250	255		
att gaa aat tct tgt gat cca gta ctt gat ctg cat atg tct ctg gag				1113
Ile Glu Asn Ser Cys Asp Pro Val Leu Asp Leu His Met Ser Leu Glu				
260	265	270		
gaa cta tat acc cag aat ctc ctg gaa aga cag gat gag aat aca cct				1161
Glu Leu Tyr Thr Gln Asn Leu Leu Glu Arg Gln Asp Glu Asn Thr Pro				
275	280	285	290	
tcg gtg gac ata agt atg ggg cct gct tct ggc ttt act ata aat gac				1209
Ser Val Asp Ile Ser Met Gly Pro Ala Ser Gly Phe Thr Ile Asn Asp				
295	300	305		
tac aca cct gca aat gct att gaa caa caa tat gaa tgt gaa aac aca				1257

00502600-00400

310

320

Ile Val Trp Thr Glu Ser His Leu Pro Ser Glu Val Ile Ser Ser Ala

335

Glu Leu Pro Ser Val Leu Pro Asp Ser Ala Gly Lys Gly Ser Glu His

350

Leu Leu Glu Gln Ser Ser Leu Ala Cys Asn Ala Glu Cys Val Met Leu

370

Gln Asn Val Ser Lys Glu Ser Phe Glu Arg Thr Ile Asn Ile Ala Lys

385

Gly Asn Ser Ser Leu Gly Met Thr Val Ser Ala Asn Lys Asp Gly Leu

400

Gly Met Ile Val Arg Ser Ile Ile His Gly Gly Ala Ile Ser Arg Asp

415



420

435 440 445 450

455

470

485 **490** **495**

500

515 520 525 530

545

560

575

590

610

625

Val Asp Lys Glu Asp Glu Phe Gly Tyr Ser Trp Lys Asn Ile Arg Glu

630

635

640

cgt tat gga acc cta aca ggc gag ctg cat atg att gaa ctg gag aaa 2265

Arg Tyr Gly Thr Leu Thr Gly Glu Leu His Met Ile Glu Leu Glu Lys

645

650

655

ggt cat agt ggt ttg ggc cta agt ctt gct ggg aac aaa gac cga tcc 2313

Gly His Ser Gly Leu Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser

660

665

670

agg atg agt gtc ttc ata gtg ggg att gat cca aat gga gct gca gga 2361

Arg Met Ser Val Phe Ile Val Gly Ile Asp Pro Asn Gly Ala Ala Gly

675

680

685

690

aaa gat ggt cga ttg caa att gca gat gag ctt cta gag atc aat ggt 2409

Lys Asp Gly Arg Leu Gln Ile Ala Asp Glu Leu Leu Glu Ile Asn Gly

695

700

705

cag att tta tat gga aga agt cat cag aat gcc tca tca atc att aaa 2457

Gln Ile Leu Tyr Gly Arg Ser His Gln Asn Ala Ser Ser Ile Ile Lys

710

715

720

tgt gcc cct tct aaa gtg aaa ata att ttt atc aga aat aaa gat gca 2505

Cys Ala Pro Ser Lys Val Lys Ile Ile Phe Ile Arg Asn Lys Asp Ala

725

730

735

gtg aat cag atg gcc gta tgt cct gga aat gca gta gaa cct ttg cct 2553

001120" 05020500

750

770

785

- 800

815

830

850

ctt ctg aag aca gca aag atg aca gta aaa ctt acc atc cat gct gag 2889
 Leu Leu Lys Thr Ala Lys Met Thr Val Lys Leu Thr Ile His Ala Glu

855

860

865

aat cca gat tcc cag gct gtt cct tca gca gct ggt gca gcc agt gga 2937
 Asn Pro Asp Ser Gln Ala Val Pro Ser Ala Ala Gly Ala Ala Ser Gly

870

875

880

gaa aaa aag aac agc tcc cag tct ctg atg gtc cca cag tct ggc tcc 2985
 Glu Lys Lys Asn Ser Ser Gln Ser Leu Met Val Pro Gln Ser Gly Ser

885

890

895

cca gaa ccg gag tcc atc cga aat aca agc aga tca tca aca cca gca 3033
 Pro Glu Pro Glu Ser Ile Arg Asn Thr Ser Arg Ser Ser Thr Pro Ala

900

905

910

att ttt gct tct gat cct gca acc tgc ccc att atc cct ggc tgc gaa 3081
 Ile Phe Ala Ser Asp Pro Ala Thr Cys Pro Ile Ile Pro Gly Cys Glu

915

920

925

930

aca acc atc gag att tcc aaa ggg cga aca ggg ctg ggc ctg agc atc 3129
 Thr Thr Ile Glu Ile Ser Lys Gly Arg Thr Gly Leu Gly Leu Ser Ile

935

940

945

gtt ggg ggt tca gac acg ctg ctg ggt gcc ttt att atc cat gaa gtt 3177
 Val Gly Gly Ser Asp Thr Leu Leu Gly Ala Phe Ile Ile His Glu Val

950

955

960

001120-252550

975

990

1010

1025

1040

1055

Lys Gly Gly Ile Ala Asp Pro Asp Gly Arg Leu Ile Gln Gly Asp Gln

1060	1065	1070	
ata tta ttg gtg aat ggg gaa gac gtt cgt aat gcc tcc caa gaa gcg			3561
Ile Leu Leu Val Asn Gly Glu Asp Val Arg Asn Ala Ser Gln Glu Ala			
1075	1080	1085	1090
gtt gcc gct ttg cta aag tgt tcc cta ggc aca gta acc ttg gaa gtt			3609
Val Ala Ala Leu Leu Lys Cys Ser Leu Gly Thr Val Thr Leu Glu Val			
1095	1100	1105	
gga aga atc aaa gct ggt cca ttc cat tca gag agg agg cca tct caa			3657
Gly Arg Ile Lys Ala Gly Pro Phe His Ser Glu Arg Arg Pro Ser Gln			
1110	1115	1120	
acc agc cag gtg agt gaa ggc agc ctg tct tct ttc act ttt cca ctc			3705
Thr Ser Gln Val Ser Glu Gly Ser Leu Ser Ser Phe Thr Phe Pro Leu			
1125	1130	1135	
tct gga tcc agt aca tct gag tca ctg gaa agt agc tca aag aag aat			3753
Ser Gly Ser Ser Thr Ser Glu Ser Leu Glu Ser Ser Ser Lys Lys Asn			
1140	1145	1150	
gca ttg gca tct gaa ata cag gga tta aga aca gtc gaa atg aaa aag			3801
Ala Leu Ala Ser Glu Ile Gln Gly Leu Arg Thr Val Glu Met Lys Lys			
1155	1160	1165	1170
ggc cct act gac tca ctg gga atc agc atc gct gga gga gta ggc agc			3849

1185

1200

1215

1230

1250

1265

1280

1285 1290 1295

1300

1315 1320 1325 1330

1335

1350

1365 1370

tttatgctgt gttcagccgg gtcttcaaaa ctgtaggggg gaaataacac ttaagtttct 4550

50

65 70 75 80

85 90

<213> Homo sapience

1 5 10 15

20 25 30

35 40 45

50

65 70 75 80

85 90

<212> PRT

<400> 6

Asn	Gln	Pro	Arg	Arg	Val	Glu	Leu	Trp	Arg	Glu	Pro	Ser	Lys	Ser	Leu
1				5					10					15	
Gly	Ile	Ser	Ile	Val	Gly	Gly	Arg	Gly	Met	Gly	Ser	Arg	Leu	Ser	Asn
				20					25					30	
Gly	Glu	Val	Met	Arg	Gly	Ile	Phe	Ile	Lys	His	Val	Leu	Glu	Asp	Ser
				35					40					45	
Pro	Ala	Gly	Lys	Asn	Gly	Thr	Leu	Lys	Pro	Gly	Asp	Arg	Ile	Val	Glu
				50					55					60	
Ala	Pro	Ser	Gln	Ser	Glu	Ser	Glu	Pro	Glu	Lys	Ala	Pro	Leu	Cys	Ser
				65					70					75	
Val	Pro	Pro	Pro	Pro	Pro	Ser	Ala	Phe	Ala	Glu	Met	Gly	Ser	Asp	His
				85					90					95	

<210> 7

<211> 86

<212> PRT

<213> Homo sapience

<400> 7

Gly Glu Leu His Met Ile Glu Leu Glu Lys Gly His Ser Gly Leu Gly
1 5 10 15
Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser Arg Met Ser Val Phe Ile
20 25 30
Val Gly Ile Asp Pro Asn Gly Ala Ala Gly Lys Asp Gly Arg Leu Gln

85

<211> 84

<213> Homo sapience

Lys Asn Val Gln His Leu Glu Leu Pro Lys Asp Gln Gly Gly Leu Gly

20 25 30

35 40 45

Asp Gln Ile Leu Ala Val Asp Asp Glu Ile Val Val Gly Tyr Pro Ile

65 70 75 80

<210> 9

<212> PRT

<213> Homo sapience

<400> 9

1 5 10 15

20 25 30

35 40 45

50 **55** **60**

65 70 75 80

85

<210> 10

<211> 85

<212> PRT

<213> Homo sapience

<400> 10

1 5 10 15

Gly Leu Ser Ile Val Gly Lys Arg Asn Asp Thr Gly Val Phe Val Ser

20 25 30
 Asp Ile Val Lys Gly Gly Ile Ala Asp Pro Asp Gly Arg Leu Ile Gln
 35 40 45
 Gly Asp Gln Ile Leu Leu Val Asn Gly Glu Asp Val Arg Asn Ala Ser
 50 55 60
 Gln Glu Ala Val Ala Ala Leu Leu Lys Cys Ser Leu Gly Thr Val Thr
 65 70 75 80
 Leu Glu Val Gly Arg
 85

<210> 11
 <211> 89
 <212> PRT
 <213> Homo sapience

<400> 11
 Gln Gly Leu Arg Thr Val Glu Met Lys Lys Gly Pro Thr Asp Ser Leu
 1 5 10 15
 Gly Ile Ser Ile Ala Gly Gly Val Gly Ser Pro Leu Gly Asp Val Pro
 20 25 30
 Ile Phe Ile Ala Met Met His Pro Thr Gly Val Ala Ala Gln Thr Gln
 35 40 45
 Lys Leu Arg Val Gly Asp Arg Ile Val Thr Ile Cys Gly Thr Ser Thr
 50 55 60
 Glu Gly Met Thr His Thr Gln Ala Val Asn Leu Leu Lys Asn Ala Ser
 65 70 75 80
 Gly Ser Ile Glu Met Gln Val Val Ala

001120 36920560

<211> 88

<212> PRT

<213> Homo sapience

<400> 12

Pro Gln Cys Lys Ser Ile Thr Leu Glu Arg Gly Pro Asp Gly Leu Gly

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Phe Ser Ile Val Gly Gly Tyr Gly Ser Pro His Gly Asp Leu Pro Ile

20 25 30

Tyr Val Lys Thr Val Phe Ala Lys Gly Ala Ala Ser Glu Asp Gly Arg

35 40 45

Leu Lys Arg Gly Asp Gln Ile Ile Ala Val Asn Gly Gln Ser Leu Glu

50 55 60

Gly Val Thr His Glu Glu Ala Val Ala Ile Leu Lys Arg Thr Lys Gly

65 70 75 80

Thr Val Thr Leu Met Val Leu Ser

85

<210> 13

<211> 184

<212> DNA

<213> Homo sapience

<400> 132

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ctccccatcc ctcggtccacc                20
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<223> Artificially Synthesized Primer Sequence

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<400> 15
ctctgactct gactgactgg                                20
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<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 18

agtcttgctg ggaacaaaga

20

<210> 19

<211> 20

<212> DNA

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actgttacta cttctgatgc

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<210> 20

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<212> DNA

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<400> 20

tctgatggtc ccacagtctg

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<210> 21

<211> 20

<212> DNA

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<223> Artificially Synthesized Primer Sequence

<400> 21

gttgtttcgc agccaggat

20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Artificially Synthesized Primer Sequence

<400> 22

ctgagcatcg ttgggggttc

20

<210> 23

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<212> DNA

<213> Artificial Sequence

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<223> Artificially Synthesized Primer Sequence

cctcatctct gtagagtgtc

20

<211> 20

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tgttagcccc ctcactaagg

20

<211> 20

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<400> 25

gctatgtgct aggaaatag

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<210> 26

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<400> 26

tagggagaag gatcagagcg

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<210> 27

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<400> 27

acagatttct gactcactgg

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<400> 35

tcctcctttg acaatgtctg

20

<210> 36

<211> 20

<212> DNA

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<400> 36

catttcgact gttcttaatc

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<210> 37

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<400> 37

tcagtggatg tgccacagat

20

<210> 38

005259-0240

<211> 20

<212> DNA

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<400> 38

cagtaggtta actgcttcgg

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<210> 39

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agttccagtc tttctttcgg

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<210> 40

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<212> DNA

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<400> 42

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<211> 20

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tcactttaga aggggcacat

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<210> 50

<211> 20

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<223> Artificially Synthesized Primer Sequence

<400> 50

actgttacta cttctgatgc

20

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Artificially Synthesized Primer Sequence

<400> 51

tctgatggtc ccacagtctg

20

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<211> 20

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<400> 54

20

<210> 55

<211> 20

<212> DNA

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<400> 55

tagggagaag gatcagagcg

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<210> 56

<211> 20

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<223> Artificially Synthesized Primer Sequence

<400> 56

tcctccttg acaatgtctg

20

<210> 57

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Artificially Synthesized Primer Sequence

001120-20920500

tttcatcatc tacagccagt

20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 58

tgacaccctc actattgagc

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<210> 59

<211> 2819

<212> DNA

<213> Homo sapience

<220>

<221> CDS

<222> (43)...(2331)

<400> 59

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54

Met Gly Ser Asn

cac aca cag tca tct gca agc aaa atc tca caa gat gtg gac aaa gag 102

His Thr Gln Ser Ser Ala Ser Lys Ile Ser Gln Asp Val Asp Lys Glu

5 10 15 20

gat gag ttt ggt tac agc tgg aaa aat atc aga gag cgt tat gga acc 150

Asp Glu Phe Gly Tyr Ser Trp Lys Asn Ile Arg Glu Arg Tyr Gly Thr

25 30 35

cta aca ggc gag ctg cat atg att gaa ctg gag aaa ggt cat agt ggt 198

Leu Thr Gly Glu Leu His Met Ile Glu Leu Glu Lys Gly His Ser Gly

40 45 50

ttg ggc cta agt ctt gct ggg aac aaa gac cga tcc agg atg agt gtc 246

Leu Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser Arg Met Ser Val

55 60 65

ttc ata gtg ggg att gat cca aat gga gct gca gga aaa gat ggt cga 294

Phe Ile Val Gly Ile Asp Pro Asn Gly Ala Ala Gly Lys Asp Gly Arg

70 75 80

ttg caa att gca gat gag ctt cta gag atc aat ggt cag att tta tat 342

Leu Gln Ile Ala Asp Glu Leu Leu Glu Ile Asn Gly Gln Ile Leu Tyr

85 90 95 100

gga aga agt cat cag aat gcc tca tca atc att aaa tgt gcc cct tct 390

Gly Arg Ser His Gln Asn Ala Ser Ser Ile Ile Lys Cys Ala Pro Ser

000000-000000

115

130

145

160

180

195

210

gat gga cga ctc aaa gtc gga gat cag ata ctg gct gta gat gat gaa

225

240

260

275

290

305

320

att tcc aaa ggg cga aca ggg ctg ggc ctg agc atc gtt ggg ggt tca 1062

Ile Ser Lys Gly Arg Thr Gly Leu Gly Leu Ser Ile Val Gly Gly Ser

325

330

335

340

gac acg ctg ctg ggt gcc ttt att atc cat gaa gtt tat gaa gaa gga 1110

Asp Thr Leu Leu Gly Ala Phe Ile Ile His Glu Val Tyr Glu Glu Gly

345

350

355

gca gca tgt aaa gat gga aga ctc tgg gct gga gat cag atc tta gag 1158

Ala Ala Cys Lys Asp Gly Arg Leu Trp Ala Gly Asp Gln Ile Leu Glu

360

365

370

gtg aat gga att gac ttg agg aag gcc aca cat gat gaa gca atc aat 1206

Val Asn Gly Ile Asp Leu Arg Lys Ala Thr His Asp Glu Ala Ile Asn

375

380

385

gtc ctg aga cag acg cca cag aga gtg cgc ctg aca ctc tac aga gat 1254

Val Leu Arg Gln Thr Pro Gln Arg Val Arg Leu Thr Leu Tyr Arg Asp

390

395

400

gag gcc cca tac aaa gag gag gaa gtg tgt gac acc ctc act att gag 1302

Glu Ala Pro Tyr Lys Glu Glu Glu Val Cys Asp Thr Leu Thr Ile Glu

405

410

415

420

ctg cag aag aag ccg gga aaa ggc cta gga tta agt att gtt ggt aaa 1350

Leu Gln Lys Lys Pro Gly Lys Gly Leu Gly Leu Ser Ile Val Gly Lys

425

430

435

00502699:021400

450

465

480

500

515

530

Thr Ser Glu Ser Leu Glu Ser Ser Ser Lys Lys Asn Ala Leu Ala Ser

535

540

545

gaa ata cag gga tta aga aca gtc gaa atg aaa aag ggc cct act gac 1734

Glu Ile Gln Gly Leu Arg Thr Val Glu Met Lys Lys Gly Pro Thr Asp

550

555

560

tca ctg gga atc agc atc gct gga gga gta ggc agc cca ctt ggt gat 1782

Ser Leu Gly Ile Ser Ile Ala Gly Gly Val Gly Ser Pro Leu Gly Asp

565

570

575

580

gtg cct ata ttt att gca atg atg cac cca act gga gtt gca gca cag 1830

Val Pro Ile Phe Ile Ala Met Met His Pro Thr Gly Val Ala Ala Gln

585

590

595

acc caa aaa ctc aga gtt ggg gat agg att gtc acc atc tgt ggc aca 1878

Thr Gln Lys Leu Arg Val Gly Asp Arg Ile Val Thr Ile Cys Gly Thr

600

605

610

tcc act gag ggc atg act cac acc caa gca gtt aac cta ctg aaa aat 1926

Ser Thr Glu Gly Met Thr His Thr Gln Ala Val Asn Leu Leu Lys Asn

615

620

625

gca tct ggc tcc att gaa atg cag gtg gtt gct gga gga gac gtg agt 1974

Ala Ser Gly Ser Ile Glu Met Gln Val Val Ala Gly Gly Asp Val Ser

630

635

640

gtg gtc aca ggt cat cat cag gag cct gca agt tcc agt ctt tct ttc 2022

Val Val Thr Gly His His Gln Glu Pro Ala Ser Ser Ser Leu Ser Phe

001120-00000000

645	650	655	660	
act ggg ctg acg tca acc agt ata ttt cag gat gat tta gga cct cct				2070
Thr Gly Leu Thr Ser Thr Ser Ile Phe Gln Asp Asp Leu Gly Pro Pro				
665	670	675		
caa tgt aag tct att aca cta gag cga gga cca gat ggc tta ggc ttc				2118
Gln Cys Lys Ser Ile Thr Leu Glu Arg Gly Pro Asp Gly Leu Gly Phe				
680	685	690		
agt ata gtt gga gga tat ggc agc cct cat gga gac tta ccc att tat				2166
Ser Ile Val Gly Gly Tyr Gly Ser Pro His Gly Asp Leu Pro Ile Tyr				
695	700	705		
gtt aaa aca gtg ttt gca aag gga gca gcc tct gaa gac gga cgt ctg				2214
Val Lys Thr Val Phe Ala Lys Gly Ala Ala Ser Glu Asp Gly Arg Leu				
710	715	720		
aaa agg ggc gat cag atc att gct gtc aat ggg cag agt cta gaa gga				2262
Lys Arg Gly Asp Gln Ile Ile Ala Val Asn Gly Gln Ser Leu Glu Gly				
725	730	735	740	
gtc acc cat gaa gaa gct gtt gcc atc ctt aaa cgg aca aaa ggc act				2310
Val Thr His Glu Glu Ala Val Ala Ile Leu Lys Arg Thr Lys Gly Thr				
745	750	755		
gtc act ttg atg gtt ctc tct tgaattggct gccagaattg aaccaaccca				2361

760

tcctctcccc accccaaact aaaaaaaaaa aaaaaaaaaa 2819

<223> Artificially Synthesized Primer Sequence

25

<213> Artificial Sequence

<223> Artificially Synthesized Primer Sequence

25

<213> Artificial Sequence

<223> Artificially Synthesized Primer Sequence

25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 63

ggcataactt tacttacttg

20

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 64

atctactaag tcagcatcat

20

<210> 65

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

00112233445566778899

atttgcaggt gtgtagtcac

20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 66

ttccttctgt gctacccgat

20

<210> 67

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 67

ggactatctt ccagaacatg

20

<210> 68

<220>

<223> Artificially Synthesized Primer Sequence

<400> 7

atcgatgggt agtaatcaca cacag

25

<210> 71

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 71

aattgctata ctggatccag agagtgg

27

<210> 72

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Peptide Sequence

<400> 72

Val Asp Lys Glu Asp Glu Phe Gly Tyr Ser Trp Lys Asn Ile Arg Glu

1

5

10

15

001120-00920560

20

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Artificially Synthesized Primer Sequence

<400> 73

tttgtgccca ccagagccaa gtcag

25

<210> 74

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 74

gtgaaagggg taaaggctta gcaac

25

<210> 75

<211> 1776

<213> Homo sapience

ca att aca cat cag cag gct atc agc atc ctg cag aaa gcc aaa gat 47

1 5 10 15

Thr Val Gln Leu Val Ile Ala Arg Gly Ser Leu Pro Gln Leu Val Ser

20 25 30

Pro Ile Val Ser Arg Ser Pro Ser Ala Ala Ser Thr Ile Ser Ala His

35 40 45

Ser Asn Pro Val His Trp Gln His Met Glu Thr Ile Glu Leu Val Asn

50 55 60

Asp Gly Ser Gly Leu Gly Phe Gly Ile Ile Gly Gly Lys Ala Thr Gly

65 **70** **75**

Val Ile Val Lys Thr Ile Leu Pro Gly Gly Val Ala Asp Gln His Gly

80 85 90 95

Arg Leu Cys Ser Gly Asp His Ile Leu Lys Ile Gly Asp Thr Asp Leu

110

Ala Gly Met Ser Ser Glu Gln Val Ala Gln Val Leu Arg Gln Cys Gly

125

Asn Arg Val Lys Leu Met Ile Ala Arg Ser Ala Ile Glu Glu Arg Thr

140

Ala Pro Thr Ala Leu Gly Ile Thr Leu Ser Ser Ser Pro Thr Ser Thr

155

Pro Glu Leu Arg Val Asp Ala Ser Thr Gln Lys Gly Glu Glu Ser Glu

175

Thr Phe Asp Val Glu Leu Thr Lys Asn Val Gln Gly Leu Gly Ile Thr

190

Ile Ala Gly Tyr Ile Gly Asp Lys Lys Leu Glu Pro Ser Gly Ile Phe

[illegible]

315

335

350

365

380

395

415

gtg gtg aat atc tta aaa gaa ctg cct ata gaa gtg aca atg gtg tgc	1295
Val Val Asn Ile Leu Lys Glu Leu Pro Ile Glu Val Thr Met Val Cys	
420 425 430	
tgt cgt cga act gtg cca ccc acc acc caa tca gaa ttg gat agc ctg	1343
Cys Arg Arg Thr Val Pro Pro Thr Thr Gln Ser Glu Leu Asp Ser Leu	
435 440 445	
gac tta tgt gat att gag cta aca gaa aag cct cac gta gat cta ggt	1391
Asp Leu Cys Asp Ile Glu Leu Thr Glu Lys Pro His Val Asp Leu Gly	
450 455 460	
gag ttc atc ggg tca tca gag cca gag gat cca gtg ctg gcg atg act	1439
Glu Phe Ile Gly Ser Ser Glu Pro Glu Asp Pro Val Leu Ala Met Thr	
465 470 475	
gat gcg ggt cag agt aca gaa gag gtt caa gca cct ttg gcc atg tgg	1487
Asp Ala Gly Gln Ser Thr Glu Glu Val Gln Ala Pro Leu Ala Met Trp	
480 485 490 495	
gag gct ggc att cag cac ata atg ctg gag aaa ggg agc aaa gga ctt	1535
Glu Ala Gly Ile Gln His Ile Met Leu Glu Lys Gly Ser Lys Gly Leu	
500 505 510	
ggt ttt agc att tta gat tat cag gat cca att gat cca gca agc act	1583
Gly Phe Ser Ile Leu Asp Tyr Gln Asp Pro Ile Asp Pro Ala Ser Thr	
515 520 525	

Val Ile Ile Ile Arg Ser Leu Val Pro Gly Gly Ile Ala Glu Lys Asp

540

Gly Arg Leu Leu Pro Gly Asp Arg Leu Met Phe Val Asn Asp Val Asn

555

Leu Glu Asn Ser Ser Leu Glu Glu Ala Val Glu Ala Leu Lys Gly Ala

575

Pro Ser Gly Thr Val Arg Ile Gly Val Ala Lys Pro Leu Pro Leu

590

1776

<213> Artificial Sequence

<223> Artificially Synthesized Primer Sequence

<400> 76

gcagatggag aacgggaaac tatgg

76

<210> 77

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 77

gaacgggaaa ctatggggct gacaa

25

<210> 78

<211> 777

<212> DNA

<213> Homo sapience

<400> 78

ttctcagtca cgcagttcca ttttaattgc tgттаатсat ttcagagaag aacactgaac

60

tttgaaaaaa atg ttg gaa gcc att gac aaa aat cgg gcc ctg cat gca

109

Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

1

5

10

00502698-021400

15 **20** **25**

30 35 40 45

50 55 60

65 70 75

80 85 90

95 100 105

110 115 120 125

140

155

170 .

185

205

220

Arg Gly Ser Leu Pro Gln Leu Val Ser Pro Ile Val Ser Arg

225

230

235

tc

777

<210> 79

<211> 755

<212> DNA

<213> Homo sapience

<400> 79

tt cct tct gtg cta ccc gat tca gct gga aag ggc tct gag tac ctg 47

Pro Ser Val Leu Pro Asp Ser Ala Gly Lys Gly Ser Glu Tyr Leu

1

5

10

15

ctt gaa cag agc tcc ctg gcc tgt aat gct gag tgt gtc atg ctt caa 95

Leu Glu Gln Ser Ser Leu Ala Cys Asn Ala Glu Cys Val Met Leu Gln

20

25

30

aat gta tct aaa gaa tct ttt gaa agg act att aat ata gca aaa ggc 143

Asn Val Ser Lys Glu Ser Phe Glu Arg Thr Ile Asn Ile Ala Lys Gly

35

40

45

aat tct agc cta gga atg aca gtt agt gct aat aaa gat ggc ttg ggg 191

Asn Ser Ser Leu Gly Met Thr Val Ser Ala Asn Lys Asp Gly Leu Gly

50

55

60

00502698-02400

65 **70** **75**

80 85 90 95

100 105 110

115

. 130 135 140

[illegible]

160 165 170 175

tat agc aat tgg aat cag ccc agg cgg gtg gaa ctc tgg aga gaa cca 575

Tyr Ser Asn Trp Asn Gln Pro Arg Arg Val Glu Leu Trp Arg Glu Pro

180

185

190

agc aaa tcc tta ggc atc agc att gtt ggt gga cga ggg atg ggg agt 623

Ser Lys Ser Leu Gly Ile Ser Ile Val Gly Gly Arg Gly Met Gly Ser

195

200

205

cgg cta agc aat gga gaa gtg atg agg ggc att ttc atc aaa cat gtt 671

Arg Leu Ser Asn Gly Glu Val Met Arg Gly Ile Phe Ile Lys His Val

210

215

220

ctg gaa gat agt cca gct ggc aaa aat gga acc ttg aaa cct gga gat 719

Leu Glu Asp Ser Pro Ala Gly Lys Asn Gly Thr Leu Lys Pro Gly Asp

225

230

235

aga atc gta gag gca ccc agt cag tca gag tca gag 755

Arg Ile Val Glu Ala Pro Ser Gln Ser Glu Ser Glu

240

245

250

<210> 80

<211> 865

<212> DNA

<213> Homo sapience

<400> 80

001120-2020500

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Pro Ser Val Leu Pro Asp Ser Ala Gly Lys Gly Ser Glu Tyr Leu

1 5 10 15

ctt gaa cag agc tcc ctg gcc tgt aat gct gag tgt gtc atg ctt caa 95

Leu Glu Gln Ser Ser Leu Ala Cys Asn Ala Glu Cys Val Met Leu Gln

20 25 30

aat gta tct aaa gaa tct ttt gaa agg act att aat ata gca aaa ggc 143

Asn Val Ser Lys Glu Ser Phe Glu Arg Thr Ile Asn Ile Ala Lys Gly

35 40 45

aat tct agc cta gga atg aca gtt agt gct aat aaa gat ggc ttg ggg 191

Asn Ser Ser Leu Gly Met Thr Val Ser Ala Asn Lys Asp Gly Leu Gly

50 55 60

atg atc gtt cga agc att att cat gga ggt gcc att agt cga gat ggc 239

Met Ile Val Arg Ser Ile Ile His Gly Gly Ala Ile Ser Arg Asp Gly

65 70 75

cgg att gcc att ggg gac tgc atc ttg tcc att aat gaa gag tct acc 287

Arg Ile Ala Ile Gly Asp Cys Ile Leu Ser Ile Asn Glu Glu Ser Thr

80 85 90 95

atc agt gta acc aat gcc cag gca cga gct atg ttg aga aga cat tct 335

Ile Ser Val Thr Asn Ala Gln Ala Arg Ala Met Leu Arg Arg His Ser

100 105 110

001100 001100 001100 001100 001100 001100 001100 001100 001100 001100

125

140

155

175

190

205

Arg Leu Ser Asn Gly Glu Val Met Arg Gly Ile Phe Ile Lys His Val

220

235

255

270

285

ag 865

<213> Homo sapience

tt cct tct gtg cta ccc gat tca gct gga aag ggc tct gag tac ctg 47

Pro Ser Val Leu Pro Asp Ser Ala Gly Lys Gly Ser Glu Tyr Leu

1 5 10 15

ctt gaa cag agc tcc ctg gcc tgt aat gct gag tgt gtc atg ctt caa 95

Leu Glu Gln Ser Ser Leu Ala Cys Asn Ala Glu Cys Val Met Leu Gln

20 25 30

aat gta tct aaa gaa tct ttt gaa agg act att aat ata gca aaa ggc 143

Asn Val Ser Lys Glu Ser Phe Glu Arg Thr Ile Asn Ile Ala Lys Gly

35 40 45

aat tct agc cta gga atg aca gtt agt gct aat aaa gat ggc ttg ggc 191

Asn Ser Ser Leu Gly Met Thr Val Ser Ala Asn Lys Asp Gly Leu Gly

50 55 60

atg atc gtt cga agc att att cat gga ggt gcc att agt cga gat ggc 239

Met Ile Val Arg Ser Ile Ile His Gly Gly Ala Ile Ser Arg Asp Gly

65 70 75

cgg att gcc att ggg gac tgc atc ttg tcc att aat gaa gag tct acc 287

Arg Ile Ala Ile Gly Asp Cys Ile Leu Ser Ile Asn Glu Glu Ser Thr

80 85 90 95

atc agt gta acc aat gcc cag gca cga gct atg ttg aga aga cat tct 335

Ile Ser Val Thr Asn Ala Gln Ala Arg Ala Met Leu Arg Arg His Ser

100 105 110

0050669-024100

115 120 125

130

145

160 165 170 175

180

195

210

ctg gaa gat agt cca gct ggc aaa aat gga acc ttg aaa cct gga gat 719

Leu Glu Asp Ser Pro Ala Gly Lys Asn Gly Thr Leu Lys Pro Gly Asp

225

230

235

aga atc gta gag gtg gat gga atg gac ctc aga gat gca agc cat gaa 767

Arg Ile Val Glu Val Asp Gly Met Asp Leu Arg Asp Ala Ser His Glu

240

245

250

255

caa gct gtg gaa gcc att cgg aaa gca ggc aac cct gta gtc ttt atg 815

Gln Ala Val Glu Ala Ile Arg Lys Ala Gly Asn Pro Val Val Phe Met

260

265

270

gta cag agc att ata aac aga cca agg aaa tcc cct ttg cct tcc ttg 863

Val Gln Ser Ile Ile Asn Arg Pro Arg Lys Ser Pro Leu Pro Ser Leu

275

280

285

ctg cac aac ctt tac cct aag tac aac ttc agc agc act aac cca ttt 911

Leu His Asn Leu Tyr Pro Lys Tyr Asn Phe Ser Ser Thr Asn Pro Phe

290

295

300

gct gac tct cta caa atc aac gcc gac aag gca ccc agt cag tca gag 959

Ala Asp Ser Leu Gln Ile Asn Ala Asp Lys Ala Pro Ser Gln Ser Glu

305

310

315

tca gag 965

Ser Glu

005055-00100

<210> 82

<211> 2000

<212> PRT

<213> Homo sapience

<400> 82

Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

1

5

10⁵

Ala Glu Arg Leu Gln Thr Lys Leu Arg Glu Arg Gly Asp Val Ala Asn

15

20

25

Glu Asp Lys Leu Ser Leu Leu Lys Ser Val Leu Gln Ser Pro Leu Phe

30

35

40

45

Ser Gln Ile Leu Ser Leu Gln Thr Ser Val Gln Gln Leu Lys Asp Gln

50

55

60

Val Asn Ile Ala Thr Ser Ala Thr Ser Asn Ile Glu Tyr Ala His Val

65

70

75

Pro His Leu Ser Pro Ala Val Ile Pro Thr Leu Gln Asn Glu Ser Phe

80

85

90

Leu Leu Ser Pro Asn Asn Gly Asn Leu Glu Ala Leu Thr Gly Pro Gly

95

100

105

Ile Pro His Ile Asn Gly Lys Pro Ala Cys Asp Glu Phe Asp Gln Leu

110

115

120

125

Ile Lys Asn Met Ala Gln Gly Arg His Val Glu Val Phe Glu Leu Leu

130

135

140

Lys Pro Pro Ser Gly Gly Leu Gly Phe Ser Val Val Gly Leu Arg Ser

	145		150		155										
Glu	Asn	Arg	Gly	Glu	Leu	Gly	Ile	Phe	Val	Gln	Glu	Ile	Gln	Glu	Gly
	160						165						170		
Ser	Val	Ala	His	Arg	Asp	Gly	Arg	Leu	Lys	Glu	Thr	Asp	Gln	Ile	Leu
	175						180						185		
Ala	Ile	Asn	Gly	Gln	Ala	Leu	Asp	Gln	Thr	Ile	Thr	His	Gln	Gln	Ala
	190					195					200				205
Ile	Ser	Ile	Leu	Gln	Lys	Ala	Lys	Asp	Thr	Val	Gln	Leu	Val	Ile	Ala
				210					215					220	
Arg	Gly	Ser	Leu	Pro	Gln	Leu	Val	Ser	Pro	Ile	Val	Ser	Arg	Ser	Pro
		225						230					235		
Ser	Ala	Ala	Ser	Thr	Ile	Ser	Ala	His	Ser	Asn	Pro	Val	His	Trp	Gln
	240						245					250			
His	Met	Glu	Thr	Ile	Glu	Leu	Val	Asn	Asp	Gly	Ser	Gly	Leu	Gly	Phe
	255					260					265				
Gly	Ile	Ile	Gly	Gly	Lys	Ala	Thr	Gly	Val	Ile	Val	Lys	Thr	Ile	Leu
	270				275					280					285
Pro	Gly	Gly	Val	Ala	Asp	Gln	His	Gly	Arg	Leu	Cys	Ser	Gly	Asp	His
			290						295				300		
Ile	Leu	Lys	Ile	Gly	Asp	Thr	Asp	Leu	Ala	Gly	Met	Ser	Ser	Glu	Gln
		305						310					315		
Val	Ala	Gln	Val	Leu	Arg	Gln	Cys	Gly	Asn	Arg	Val	Lys	Leu	Met	Ile
	320						325					330			
Ala	Arg	Ser	Ala	Ile	Glu	Glu	Arg	Thr	Ala	Pro	Thr	Ala	Leu	Gly	Ile
	335						340					345			
Thr	Leu	Ser	Ser	Ser	Pro	Thr	Ser	Thr	Pro	Glu	Leu	Arg	Val	Asp	Ala
	350				355					360					365

Ser	Thr	Gln	Lys	Gly	Glu	Glu	Ser	Glu	Thr	Phe	Asp	Val	Glu	Leu	Thr
				370					375					380	
Lys	Asn	Val	Gln	Gly	Leu	Gly	Ile	Thr	Ile	Ala	Gly	Tyr	Ile	Gly	Asp
				385					390					395	
Lys	Lys	Leu	Glu	Pro	Ser	Gly	Ile	Phe	Val	Lys	Ser	Ile	Thr	Lys	Ser
				400				405						410	
Ser	Ala	Val	Glu	His	Asp	Gly	Arg	Ile	Gln	Ile	Gly	Asp	Gln	Ile	Ile
				415				420						425	
Ala	Val	Asp	Gly	Thr	Asn	Leu	Gln	Gly	Phe	Thr	Asn	Gln	Gln	Ala	Val
				430				435						440	
Glu	Val	Leu	Arg	His	Thr	Gly	Gln	Thr	Val	Leu	Leu	Thr	Leu	Met	Arg
				450				455						460	
Arg	Gly	Met	Lys	Gln	Glu	Ala	Glu	Leu	Met	Ser	Arg	Glu	Asp	Val	Thr
				465				470						475	
Lys	Asp	Ala	Asp	Leu	Ser	Pro	Val	Asn	Ala	Ser	Ile	Ile	Lys	Glu	Asn
				480				485						490	
Tyr	Glu	Lys	Asp	Glu	Asp	Phe	Leu	Ser	Ser	Thr	Arg	Asn	Thr	Asn	Ile
				495				500						505	
Leu	Pro	Thr	Glu	Glu	Glu	Gly	Tyr	Pro	Leu	Leu	Ser	Ala	Glu	Ile	Glu
				510				515						520	
Glu	Ile	Glu	Asp	Ala	Gln	Lys	Gln	Glu	Ala	Ala	Leu	Leu	Thr	Lys	Trp
				530				535						540	
Gln	Arg	Ile	Met	Gly	Ile	Asn	Tyr	Glu	Ile	Val	Val	Ala	His	Val	Ser
				545				550						555	
Lys	Phe	Ser	Glu	Asn	Ser	Gly	Leu	Gly	Ile	Ser	Leu	Glu	Ala	Thr	Val
				560				565						570	
Gly	His	His	Phe	Ile	Arg	Ser	Val	Leu	Pro	Glu	Gly	Pro	Val	Gly	His

575 580 585
 Ser Gly Lys Leu Phe Ser Gly Asp Glu Leu Leu Glu Val Asn Gly Ile
 590 595 600 605
 Thr Leu Leu Gly Glu Asn His Gln Asp Val Val Asn Ile Leu Lys Glu
 610 615 620
 Leu Pro Ile Glu Val Thr Met Val Cys Cys Arg Arg Thr Val Pro Pro
 625 630 635
 Thr Thr Gln Ser Glu Leu Asp Ser Leu Asp Leu Cys Asp Ile Glu Leu
 640 645 650
 Thr Glu Lys Pro His Val Asp Leu Gly Glu Phe Ile Gly Ser Ser Glu
 655 660 665
 Pro Glu Asp Pro Val Leu Ala Met Thr Asp Ala Gly Gln Ser Thr Glu
 670 675 680 685
 Glu Val Gln Ala Pro Leu Ala Met Trp Glu Ala Gly Ile Gln His Ile
 690 695 700
 Met Leu Glu Lys Gly Ser Lys Gly Leu Gly Phe Ser Ile Leu Asp Tyr
 705 710 715
 Gln Asp Pro Ile Asp Pro Ala Ser Thr Val Ile Ile Ile Arg Ser Leu
 720 725 730
 Val Pro Gly Gly Ile Ala Glu Lys Asp Gly Arg Leu Leu Pro Gly Asp
 735 740 745
 Arg Leu Met Phe Val Asn Asp Val Asn Leu Glu Asn Ser Ser Leu Glu
 750 755 760 765
 Glu Ala Val Glu Ala Leu Lys Gly Ala Pro Ser Gly Thr Val Arg Ile
 770 775 780
 Gly Val Ala Lys Pro Leu Pro Leu Ser Pro Glu Glu Gly Tyr Val Ser
 785 790 795

005066-00400

800 805 810

815 820 825

830 835 840 845

850 855 860

865

880

895 **900** **905**

910 915 920 925

930

945

960

975 980 985

990 995 1000 1005

Glu Arg Thr Ile Asn Ile Ala Lys Gly Asn Ser Ser Leu Gly Met Thr

1010	1015	1020	
Val Ser Ala Asn Lys Asp Gly Leu Gly Met Ile Val Arg Ser Ile Ile			
1025	1030	1035	
His Gly Gly Ala Ile Ser Arg Asp Gly Arg Ile Ala Ile Gly Asp Cys			
1040	1045	1050	
Ile Leu Ser Ile Asn Glu Glu Ser Thr Ile Ser Val Thr Asn Ala Gln			
1055	1060	1065	
Ala Arg Ala Met Leu Arg Arg His Ser Leu Ile Gly Pro Asp Ile Lys			
1070	1075	1080	1085
Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu			
1090	1095	1100	
Gly Gln Gln Ser Gly Arg Val Met Ala Leu Asp Ile Phe Ser Ser Tyr			
1105	1110	1115	
Thr Gly Arg Asp Ile Pro Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly			
1120	1125	1130	
Glu Glu Ser Glu Leu Gln Asn Thr Ala Tyr Ser Asn Trp Asn Gln Pro			
1135	1140	1145	
Arg Arg Val Glu Leu Trp Arg Glu Pro Ser Lys Ser Leu Gly Ile Ser			
1150	1155	1160	1165
Ile Val Gly Gly Arg Gly Met Gly Ser Arg Leu Ser Asn Gly Glu Val			
1170	1175	1180	
Met Arg Gly Ile Phe Ile Lys His Val Leu Glu Asp Ser Pro Ala Gly			
1185	1190	1195	
Lys Asn Gly Thr Leu Lys Pro Gly Asp Arg Ile Val Glu Ala Pro Ser			
1200	1205	1210	
Gln Ser Glu Ser Glu Pro Glu Lys Ala Pro Leu Cys Ser Val Pro Pro			
1215	1220	1225	

001120 00920560

Pro	Pro	Pro	Ser	Ala	Phe	Ala	Glu	Met	Gly	Ser	Asp	His	Thr	Gln	Ser
1230						1235					1240				1245
Ser	Ala	Ser	Lys	Ile	Ser	Gln	Asp	Val	Asp	Lys	Glu	Asp	Glu	Phe	Gly
						1250					1255				1260
Tyr	Ser	Trp	Lys	Asn	Ile	Arg	Glu	Arg	Tyr	Gly	Thr	Leu	Thr	Gly	Glu
						1265					1270				1275
Leu	His	Met	Ile	Glu	Leu	Glu	Lys	Gly	His	Ser	Gly	Leu	Gly	Leu	Ser
						1280					1285				1290
Leu	Ala	Gly	Asn	Lys	Asp	Arg	Ser	Arg	Met	Ser	Val	Phe	Ile	Val	Gly
						1295					1300				1305
Ile	Asp	Pro	Asn	Gly	Ala	Ala	Gly	Lys	Asp	Gly	Arg	Leu	Gln	Ile	Ala
1310						1315					1320				1325
Asp	Glu	Leu	Leu	Glu	Ile	Asn	Gly	Gln	Ile	Leu	Tyr	Gly	Arg	Ser	His
						1330					1335				1340
Gln	Asn	Ala	Ser	Ser	Ile	Ile	Lys	Cys	Ala	Pro	Ser	Lys	Val	Lys	Ile
						1345					1350				1355
Ile	Phe	Ile	Arg	Asn	Lys	Asp	Ala	Val	Asn	Gln	Met	Ala	Val	Cys	Pro
						1360					1365				1370
Gly	Asn	Ala	Val	Glu	Pro	Leu	Pro	Ser	Asn	Ser	Glu	Asn	Leu	Gln	Asn
1375						1380					1385				
Lys	Glu	Thr	Glu	Pro	Thr	Val	Thr	Thr	Ser	Asp	Ala	Ala	Val	Asp	Leu
1390						1395					1400				1405
Ser	Ser	Phe	Lys	Asn	Val	Gln	His	Leu	Glu	Leu	Pro	Lys	Asp	Gln	Gly
						1410					1415				1420
Gly	Leu	Gly	Ile	Ala	Ile	Ser	Glu	Glu	Asp	Thr	Leu	Ser	Gly	Val	Ile
						1425					1430				1435
Ile	Lys	Ser	Leu	Thr	Glu	His	Gly	Val	Ala	Ala	Thr	Asp	Gly	Arg	Leu

1440	1445	1450
Lys Val Gly Asp Gln Ile Leu Ala Val Asp Asp Glu Ile Val Val Gly		
1455	1460	1465
Tyr Pro Ile Glu Lys Phe Ile Ser Leu Leu Lys Thr Ala Lys Met Thr		
1470	1475	1480
Val Lys Leu Thr Ile His Ala Glu Asn Pro Asp Ser Gln Ala Val Pro		
1490	1495	1500
Ser Ala Ala Gly Ala Ala Ser Gly Glu Lys Lys Asn Ser Ser Gln Ser		
1505	1510	1515
Leu Met Val Pro Gln Ser Gly Ser Pro Glu Pro Glu Ser Ile Arg Asn		
1520	1525	1530
Thr Ser Arg Ser Ser Thr Pro Ala Ile Phe Ala Ser Asp Pro Ala Thr		
1535	1540	1545
Cys Pro Ile Ile Pro Gly Cys Glu Thr Thr Ile Glu Ile Ser Lys Gly		
1550	1555	1560
Arg Thr Gly Leu Gly Leu Ser Ile Val Gly Gly Ser Asp Thr Leu Leu		
1570	1575	1580
Gly Ala Phe Ile Ile His Glu Val Tyr Glu Glu Gly Ala Ala Cys Lys		
1585	1590	1595
Asp Gly Arg Leu Trp Ala Gly Asp Gln Ile Leu Glu Val Asn Gly Ile		
1600	1605	1610
Asp Leu Arg Lys Ala Thr His Asp Glu Ala Ile Asn Val Leu Arg Gln		
1615	1620	1625
Thr Pro Gln Arg Val Arg Leu Thr Leu Tyr Arg Asp Glu Ala Pro Tyr		
1630	1635	1640
Lys Glu Glu Glu Val Cys Asp Thr Leu Thr Ile Glu Leu Gln Lys Lys		
1650	1655	1660

1675

1690

1705

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1865

Ile Glu Met Gln Val Val Ala Gly Gly Asp Val Ser Val Val Thr Gly

1870 1875 1880 1885
 His His Gln Glu Pro Ala Ser Ser Ser Leu Ser Phe Thr Gly Leu Thr
 1890 1895 1900
 Ser Thr Ser Ile Phe Gln Asp Asp Leu Gly Pro Pro Gln Cys Lys Ser
 1905 1910 1915
 Ile Thr Leu Glu Arg Gly Pro Asp Gly Leu Gly Phe Ser Ile Val Gly
 1920 1925 1930
 Gly Tyr Gly Ser Pro His Gly Asp Leu Pro Ile Tyr Val Lys Thr Val
 1935 1940 1945
 Phe Ala Lys Gly Ala Ala Ser Glu Asp Gly Arg Leu Lys Arg Gly Asp
 1950 1955 1960 1965
 Gln Ile Ile Ala Val Asn Gly Gln Ser Leu Glu Gly Val Thr His Glu
 1970 1975 1980
 Glu Ala Val Ala Ile Leu Lys Arg Thr Lys Gly Thr Val Thr Leu Met
 1985 1990 1995
 Val Leu Ser
 2000

<210> 83

<211> 2070

<212> PRT

<213> Homo sapience

<400> 83

Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

1

5

10

Ala Glu Arg Leu Gln Thr Lys Leu Arg Glu Arg Gly Asp Val Ala Asn

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15	20	25	
Glu Asp Lys Leu Ser Leu Leu Lys Ser Val Leu Gln Ser Pro Leu Phe			
30	35	40	45
Ser Gln Ile Leu Ser Leu Gln Thr Ser Val Gln Gln Leu Lys Asp Gln			
50	55	60	
Val Asn Ile Ala Thr Ser Ala Thr Ser Asn Ile Glu Tyr Ala His Val			
65	70	75	
Pro His Leu Ser Pro Ala Val Ile Pro Thr Leu Gln Asn Glu Ser Phe			
80	85	90	
Leu Leu Ser Pro Asn Asn Gly Asn Leu Glu Ala Leu Thr Gly Pro Gly			
95	100	105	
Ile Pro His Ile Asn Gly Lys Pro Ala Cys Asp Glu Phe Asp Gln Leu			
110	115	120	125
Ile Lys Asn Met Ala Gln Gly Arg His Val Glu Val Phe Glu Leu Leu			
130	135	140	
Lys Pro Pro Ser Gly Gly Leu Gly Phe Ser Val Val Gly Leu Arg Ser			
145	150	155	
Glu Asn Arg Gly Glu Leu Gly Ile Phe Val Gln Glu Ile Gln Glu Gly			
160	165	170	
Ser Val Ala His Arg Asp Gly Arg Leu Lys Glu Thr Asp Gln Ile Leu			
175	180	185	
Ala Ile Asn Gly Gln Ala Leu Asp Gln Thr Ile Thr His Gln Gln Ala			
190	195	200	205
Ile Ser Ile Leu Gln Lys Ala Lys Asp Thr Val Gln Leu Val Ile Ala			
210	215	220	
Arg Gly Ser Leu Pro Gln Leu Val Ser Pro Ile Val Ser Arg Ser Pro			
225	230	235	

Ser Ala Ala Ser Thr Ile Ser Ala His Ser Asn Pro Val His Trp Gln
 240 245 250
 His Met Glu Thr Ile Glu Leu Val Asn Asp Gly Ser Gly Leu Gly Phe
 255 260 265
 Gly Ile Ile Gly Gly Lys Ala Thr Gly Val Ile Val Lys Thr Ile Leu
 270 275 280 285
 Pro Gly Gly Val Ala Asp Gln His Gly Arg Leu Cys Ser Gly Asp His
 290 295 300
 Ile Leu Lys Ile Gly Asp Thr Asp Leu Ala Gly Met Ser Ser Glu Gln
 305 310 315
 Val Ala Gln Val Leu Arg Gln Cys Gly Asn Arg Val Lys Leu Met Ile
 320 325 330
 Ala Arg Ser Ala Ile Glu Glu Arg Thr Ala Pro Thr Ala Leu Gly Ile
 335 340 345
 Thr Leu Ser Ser Ser Pro Thr Ser Thr Pro Glu Leu Arg Val Asp Ala
 350 355 360 365
 Ser Thr Gln Lys Gly Glu Glu Ser Glu Thr Phe Asp Val Glu Leu Thr
 370 375 380
 Lys Asn Val Gln Gly Leu Gly Ile Thr Ile Ala Gly Tyr Ile Gly Asp
 385 390 395
 Lys Lys Leu Glu Pro Ser Gly Ile Phe Val Lys Ser Ile Thr Lys Ser
 400 405 410
 Ser Ala Val Glu His Asp Gly Arg Ile Gln Ile Gly Asp Gln Ile Ile
 415 420 425
 Ala Val Asp Gly Thr Asn Leu Gln Gly Phe Thr Asn Gln Gln Ala Val
 430 435 440 445
 Glu Val Leu Arg His Thr Gly Gln Thr Val Leu Leu Thr Leu Met Arg

005059-02400
 005059-02400

450 455 460
 Arg Gly Met Lys Gln Glu Ala Glu Leu Met Ser Arg Glu Asp Val Thr
 465 470 475
 Lys Asp Ala Asp Leu Ser Pro Val Asn Ala Ser Ile Ile Lys Glu Asn
 480 485 490
 Tyr Glu Lys Asp Glu Asp Phe Leu Ser Ser Thr Arg Asn Thr Asn Ile
 495 500 505
 Leu Pro Thr Glu Glu Glu Gly Tyr Pro Leu Leu Ser Ala Glu Ile Glu
 510 515 520 525
 Glu Ile Glu Asp Ala Gln Lys Gln Glu Ala Ala Leu Leu Thr Lys Trp
 530 535 540
 Gln Arg Ile Met Gly Ile Asn Tyr Glu Ile Val Val Ala His Val Ser
 545 550 555
 Lys Phe Ser Glu Asn Ser Gly Leu Gly Ile Ser Leu Glu Ala Thr Val
 560 565 570
 Gly His His Phe Ile Arg Ser Val Leu Pro Glu Gly Pro Val Gly His
 575 580 585
 Ser Gly Lys Leu Phe Ser Gly Asp Glu Leu Leu Glu Val Asn Gly Ile
 590 595 600 605
 Thr Leu Leu Gly Glu Asn His Gln Asp Val Val Asn Ile Leu Lys Glu
 610 615 620
 Leu Pro Ile Glu Val Thr Met Val Cys Cys Arg Arg Thr Val Pro Pro
 625 630 635
 Thr Thr Gln Ser Glu Leu Asp Ser Leu Asp Leu Cys Asp Ile Glu Leu
 640 645 650
 Thr Glu Lys Pro His Val Asp Leu Gly Glu Phe Ile Gly Ser Ser Glu
 655 660 665

00502599 02400

Pro	Glu	Asp	Pro	Val	Leu	Ala	Met	Thr	Asp	Ala	Gly	Gln	Ser	Thr	Glu
670					675					680					685
Glu	Val	Gln	Ala	Pro	Leu	Ala	Met	Trp	Glu	Ala	Gly	Ile	Gln	His	Ile
				690						695					700
Met	Leu	Glu	Lys	Gly	Ser	Lys	Gly	Leu	Gly	Phe	Ser	Ile	Leu	Asp	Tyr
			705						710						715
Gln	Asp	Pro	Ile	Asp	Pro	Ala	Ser	Thr	Val	Ile	Ile	Ile	Arg	Ser	Leu
		720						725					730		
Val	Pro	Gly	Gly	Ile	Ala	Glu	Lys	Asp	Gly	Arg	Leu	Leu	Pro	Gly	Asp
		735					740						745		
Arg	Leu	Met	Phe	Val	Asn	Asp	Val	Asn	Leu	Glu	Asn	Ser	Ser	Leu	Glu
750				755						760					765
Glu	Ala	Val	Glu	Ala	Leu	Lys	Gly	Ala	Pro	Ser	Gly	Thr	Val	Arg	Ile
				770						775					780
Gly	Val	Ala	Lys	Pro	Leu	Pro	Leu	Ser	Pro	Glu	Glu	Gly	Tyr	Val	Ser
			785						790						795
Ala	Lys	Glu	Asp	Ser	Phe	Leu	Tyr	Pro	Pro	His	Ser	Cys	Glu	Glu	Ala
		800							805						810
Gly	Leu	Ala	Asp	Lys	Pro	Leu	Phe	Arg	Ala	Asp	Leu	Ala	Leu	Val	Gly
		815					820								825
Thr	Asn	Asp	Ala	Asp	Leu	Val	Asp	Glu	Ser	Thr	Phe	Glu	Ser	Pro	Tyr
830					835						840				845
Ser	Pro	Glu	Asn	Asp	Ser	Ile	Tyr	Ser	Thr	Gln	Ala	Ser	Ile	Leu	Ser
				850						855					860
Leu	His	Gly	Ser	Ser	Cys	Gly	Asp	Gly	Leu	Asn	Tyr	Gly	Ser	Ser	Leu
				865						870					875
Pro	Ser	Ser	Pro	Pro	Lys	Asp	Val	Ile	Glu	Asn	Ser	Cys	Asp	Pro	Val

880	885	890
Leu Asp Leu His Met Ser Leu Glu Glu Leu Tyr Thr Gln Asn Leu Leu		
895	900	905
Glu Arg Gln Asp Glu Asn Thr Pro Ser Val Asp Ile Ser Met Gly Pro		
910	915	920
Ala Ser Gly Phe Thr Ile Asn Asp Tyr Thr Pro Ala Asn Ala Ile Glu		
930	935	940
Gln Gln Tyr Glu Cys Glu Asn Thr Ile Val Trp Thr Glu Ser His Leu		
945	950	955
Pro Ser Glu Val Ile Ser Ser Ala Glu Leu Pro Ser Val Leu Pro Asp		
960	965	970
Ser Ala Gly Lys Gly Ser Glu Tyr Leu Leu Glu Gln Ser Ser Leu Ala		
975	980	985
Cys Asn Ala Glu Cys Val Met Leu Gln Asn Val Ser Lys Glu Ser Phe		
990	995	1000
Glu Arg Thr Ile Asn Ile Ala Lys Gly Asn Ser Ser Leu Gly Met Thr		
1010	1015	1020
Val Ser Ala Asn Lys Asp Gly Leu Gly Met Ile Val Arg Ser Ile Ile		
1025	1030	1035
His Gly Gly Ala Ile Ser Arg Asp Gly Arg Ile Ala Ile Gly Asp Cys		
1040	1045	1050
Ile Leu Ser Ile Asn Glu Glu Ser Thr Ile Ser Val Thr Asn Ala Gln		
1055	1060	1065
Ala Arg Ala Met Leu Arg Arg His Ser Leu Ile Gly Pro Asp Ile Lys		
1070	1075	1080
Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu		
1090	1095	1100

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Ser Asp His Thr Gln Ser Ser Ala Ser Lys Ile Ser Gln Asp Val Asp

1310 1315 1320 1325
 Lys Glu Asp Glu Phe Gly Tyr Ser Trp Lys Asn Ile Arg Glu Arg Tyr
 1330 1335 1340
 Gly Thr Leu Thr Gly Glu Leu His Met Ile Glu Leu Glu Lys Gly His
 1345 1350 1355
 Ser Gly Leu Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser Arg Met
 1360 1365 1370
 Ser Val Phe Ile Val Gly Ile Asp Pro Asn Gly Ala Ala Gly Lys Asp
 1375 1380 1385
 Gly Arg Leu Gln Ile Ala Asp Glu Leu Leu Glu Ile Asn Gly Gln Ile
 1390 1395 1400 1405
 Leu Tyr Gly Arg Ser His Gln Asn Ala Ser Ser Ile Ile Lys Cys Ala
 1410 1415 1420
 Pro Ser Lys Val Lys Ile Ile Phe Ile Arg Asn Lys Asp Ala Val Asn
 1425 1430 1435
 Gln Met Ala Val Cys Pro Gly Asn Ala Val Glu Pro Leu Pro Ser Asn
 1440 1445 1450
 Ser Glu Asn Leu Gln Asn Lys Glu Thr Glu Pro Thr Val Thr Thr Ser
 1455 1460 1465
 Asp Ala Ala Val Asp Leu Ser Ser Phe Lys Asn Val Gln His Leu Glu
 1470 1475 1480 1485
 Leu Pro Lys Asp Gln Gly Gly Leu Gly Ile Ala Ile Ser Glu Glu Asp
 1490 1495 1500
 Thr Leu Ser Gly Val Ile Ile Lys Ser Leu Thr Glu His Gly Val Ala
 1505 1510 1515
 Ala Thr Asp Gly Arg Leu Lys Val Gly Asp Gln Ile Leu Ala Val Asp
 1520 1525 1530

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1545

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1580

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1675

1690

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Gly Lys Arg Asn Asp Thr Gly Val Phe Val Ser Asp Ile Val Lys Gly

1745	1750	1755	
Gly Ile Ala Asp Pro Asp Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu			
1760	1765	1770	
Leu Val Asn Gly Glu Asp Val Arg Asn Ala Ser Gln Glu Ala Val Ala			
1775	1780	1785	
Ala Leu Leu Lys Cys Ser Leu Gly Thr Val Thr Leu Glu Val Gly Arg			
1790	1795	1800	1805
Ile Lys Ala Gly Pro Phe His Ser Glu Arg Arg Pro Ser Gln Thr Ser			
1810	1815	1820	
Gln Val Ser Glu Gly Ser Leu Ser Ser Phe Thr Phe Pro Leu Ser Gly			
1825	1830	1835	
Ser Ser Thr Ser Glu Ser Leu Glu Ser Ser Ser Lys Lys Asn Ala Leu			
1840	1845	1850	
Ala Ser Glu Ile Gln Gly Leu Arg Thr Val Glu Met Lys Lys Gly Pro			
1855	1860	1865	
Thr Asp Ser Leu Gly Ile Ser Ile Ala Gly Gly Val Gly Ser Pro Leu			
1870	1875	1880	1885
Gly Asp Val Pro Ile Phe Ile Ala Met Met His Pro Thr Gly Val Ala			
1890	1895	1900	
Ala Gln Thr Gln Lys Leu Arg Val Gly Asp Arg Ile Val Thr Ile Cys			
1905	1910	1915	
Gly Thr Ser Thr Glu Gly Met Thr His Thr Gln Ala Val Asn Leu Leu			
1920	1925	1930	
Lys Asn Ala Ser Gly Ser Ile Glu Met Gln Val Val Ala Gly Gly Asp			
1935	1940	1945	
Val Ser Val Val Thr Gly His His Gln Glu Pro Ala Ser Ser Ser Leu			
1950	1955	1960	1965

005050-02400

1980

1995

2010

2025

2045

2060

2070

<213> Homo sapience

<400> 84

10

25

45

Ser	Gln	Ile	Leu	Ser	Leu	Gln	Thr	Ser	Val	Gln	Gln	Leu	Lys	Asp	Gln
				50					55					60	
Val	Asn	Ile	Ala	Thr	Ser	Ala	Thr	Ser	Asn	Ile	Glu	Tyr	Ala	His	Val
				65					70					75	
Pro	His	Leu	Ser	Pro	Ala	Val	Ile	Pro	Thr	Leu	Gln	Asn	Glu	Ser	Phe
		80					85					90			
Leu	Leu	Ser	Pro	Asn	Asn	Gly	Asn	Leu	Glu	Ala	Leu	Thr	Gly	Pro	Gly
		95				100					105				
Ile	Pro	His	Ile	Asn	Gly	Lys	Pro	Ala	Cys	Asp	Glu	Phe	Asp	Gln	Leu
110				115						120				125	
Ile	Lys	Asn	Met	Ala	Gln	Gly	Arg	His	Val	Glu	Val	Phe	Glu	Leu	Leu
				130					135					140	
Lys	Pro	Pro	Ser	Gly	Gly	Leu	Gly	Phe	Ser	Val	Val	Gly	Leu	Arg	Ser
			145					150					155		
Glu	Asn	Arg	Gly	Glu	Leu	Gly	Ile	Phe	Val	Gln	Glu	Ile	Gln	Glu	Gly
		160					165					170			
Ser	Val	Ala	His	Arg	Asp	Gly	Arg	Leu	Lys	Glu	Thr	Asp	Gln	Ile	Leu
		175				180						185			
Ala	Ile	Asn	Gly	Gln	Ala	Leu	Asp	Gln	Thr	Ile	Thr	His	Gln	Gln	Ala
190				195						200				205	
Ile	Ser	Ile	Leu	Gln	Lys	Ala	Lys	Asp	Thr	Val	Gln	Leu	Val	Ile	Ala
				210					215					220	
Arg	Gly	Ser	Leu	Pro	Gln	Leu	Val	Ser	Pro	Ile	Val	Ser	Arg	Ser	Pro
			225					230					235		
Ser	Ala	Ala	Ser	Thr	Ile	Ser	Ala	His	Ser	Asn	Pro	Val	His	Trp	Gln
		240				245						250			
His	Met	Glu	Thr	Ile	Glu	Leu	Val	Asn	Asp	Gly	Ser	Gly	Leu	Gly	Phe

255 260 265
 Gly Ile Ile Gly Gly Lys Ala Thr Gly Val Ile Val Lys Thr Ile Leu
 270 275 280 285
 Pro Gly Gly Val Ala Asp Gln His Gly Arg Leu Cys Ser Gly Asp His
 290 295 300
 Ile Leu Lys Ile Gly Asp Thr Asp Leu Ala Gly Met Ser Ser Glu Gln
 305 310 315
 Val Ala Gln Val Leu Arg Gln Cys Gly Asn Arg Val Lys Leu Met Ile
 320 325 330
 Ala Arg Ser Ala Ile Glu Glu Arg Thr Ala Pro Thr Ala Leu Gly Ile
 335 340 345
 Thr Leu Ser Ser Ser Pro Thr Ser Thr Pro Glu Leu Arg Val Asp Ala
 350 355 360 365
 Ser Thr Gln Lys Gly Glu Glu Ser Glu Thr Phe Asp Val Glu Leu Thr
 370 375 380
 Lys Asn Val Gln Gly Leu Gly Ile Thr Ile Ala Gly Tyr Ile Gly Asp
 385 390 395
 Lys Lys Leu Glu Pro Ser Gly Ile Phe Val Lys Ser Ile Thr Lys Ser
 400 405 410
 Ser Ala Val Glu His Asp Gly Arg Ile Gln Ile Gly Asp Gln Ile Ile
 415 420 425
 Ala Val Asp Gly Thr Asn Leu Gln Gly Phe Thr Asn Gln Gln Ala Val
 430 435 440 445
 Glu Val Leu Arg His Thr Gly Gln Thr Val Leu Leu Thr Leu Met Arg
 450 455 460
 Arg Gly Met Lys Gln Glu Ala Glu Leu Met Ser Arg Glu Asp Val Thr
 465 470 475

001120 6532330

Lys Asp Ala Asp Leu Ser Pro Val Asn Ala Ser Ile Ile Lys Glu Asn			
480	485	490	
Tyr Glu Lys Asp Glu Asp Phe Leu Ser Ser Thr Arg Asn Thr Asn Ile			
495	500	505	
Leu Pro Thr Glu Glu Glu Gly Tyr Pro Leu Leu Ser Ala Glu Ile Glu			
510	515	520	525
Glu Ile Glu Asp Ala Gln Lys Gln Glu Ala Ala Leu Leu Thr Lys Trp			
530	535	540	
Gln Arg Ile Met Gly Ile Asn Tyr Glu Ile Val Val Ala His Val Ser			
545	550	555	
Lys Phe Ser Glu Asn Ser Gly Leu Gly Ile Ser Leu Glu Ala Thr Val			
560	565	570	
Gly His His Phe Ile Arg Ser Val Leu Pro Glu Gly Pro Val Gly His			
575	580	585	
Ser Gly Lys Leu Phe Ser Gly Asp Glu Leu Leu Glu Val Asn Gly Ile			
590	595	600	605
Thr Leu Leu Gly Glu Asn His Gln Asp Val Val Asn Ile Leu Lys Glu			
610	615	620	
Leu Pro Ile Glu Val Thr Met Val Cys Cys Arg Arg Thr Val Pro Pro			
625	630	635	
Thr Thr Gln Ser Glu Leu Asp Ser Leu Asp Leu Cys Asp Ile Glu Leu			
640	645	650	
Thr Glu Lys Pro His Val Asp Leu Gly Glu Phe Ile Gly Ser Ser Glu			
655	660	665	
Pro Glu Asp Pro Val Leu Ala Met Thr Asp Ala Gly Gln Ser Thr Glu			
670	675	680	685
Glu Val Gln Ala Pro Leu Ala Met Trp Glu Ala Gly Ile Gln His Ile			

	690		695		700
Met Leu Glu Lys Gly Ser Lys Gly Leu Gly Phe Ser Ile Leu Asp Tyr					
	705		710		715
Gln Asp Pro Ile Asp Pro Ala Ser Thr Val Ile Ile Ile Arg Ser Leu					
	720		725		730
Val Pro Gly Gly Ile Ala Glu Lys Asp Gly Arg Leu Leu Pro Gly Asp					
	735		740		745
Arg Leu Met Phe Val Asn Asp Val Asn Leu Glu Asn Ser Ser Leu Glu					
	750		755		760
Glu Ala Val Glu Ala Leu Lys Gly Ala Pro Ser Gly Thr Val Arg Ile					
	770		775		780
Gly Val Ala Lys Pro Leu Pro Leu Ser Pro Glu Glu Gly Tyr Val Ser					
	785		790		795
Ala Lys Glu Asp Ser Phe Leu Tyr Pro Pro His Ser Cys Glu Glu Ala					
	800		805		810
Gly Leu Ala Asp Lys Pro Leu Phe Arg Ala Asp Leu Ala Leu Val Gly					
	815		820		825
Thr Asn Asp Ala Asp Leu Val Asp Glu Ser Thr Phe Glu Ser Pro Tyr					
	830		835		840
Ser Pro Glu Asn Asp Ser Ile Tyr Ser Thr Gln Ala Ser Ile Leu Ser					
	850		855		860
Leu His Gly Ser Ser Cys Gly Asp Gly Leu Asn Tyr Gly Ser Ser Leu					
	865		870		875
Pro Ser Ser Pro Pro Lys Asp Val Ile Glu Asn Ser Cys Asp Pro Val					
	880		885		890
Leu Asp Leu His Met Ser Leu Glu Glu Leu Tyr Thr Gln Asn Leu Leu					
	895		900		905

Glu Arg Gln Asp Glu Asn Thr Pro Ser Val Asp Ile Ser Met Gly Pro			
910	915	920	925
Ala Ser Gly Phe Thr Ile Asn Asp Tyr Thr Pro Ala Asn Ala Ile Glu			
	930	935	940
Gln Gln Tyr Glu Cys Glu Asn Thr Ile Val Trp Thr Glu Ser His Leu			
	945	950	955
Pro Ser Glu Val Ile Ser Ser Ala Glu Leu Pro Ser Val Leu Pro Asp			
	960	965	970
Ser Ala Gly Lys Gly Ser Glu His Leu Leu Glu Gln Ser Ser Leu Ala			
	975	980	985
Cys Asn Ala Glu Cys Val Met Leu Gln Asn Val Ser Lys Glu Ser Phe			
990	995	1000	1005
Glu Arg Thr Ile Asn Ile Ala Lys Gly Asn Ser Ser Leu Gly Met Thr			
	1010	1015	1020
Val Ser Ala Asn Lys Asp Gly Leu Gly Met Ile Val Arg Ser Ile Ile			
	1025	1030	1035
His Gly Gly Ala Ile Ser Arg Asp Gly Arg Ile Ala Ile Gly Asp Cys			
	1040	1045	1050
Ile Leu Ser Ile Asn Glu Glu Ser Thr Ile Ser Val Thr Asn Ala Gln			
	1055	1060	1065
Ala Arg Ala Met Leu Arg Arg His Ser Leu Ile Gly Pro Asp Ile Lys			
1070	1075	1080	1085
Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu			
	1090	1095	1100
Gly Gln Gln Ser Gly Arg Val Met Ala Leu Asp Ile Phe Ser Ser Tyr			
	1105	1110	1115
Thr Gly Arg Asp Ile Pro Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly			

<210> 85
<211> 6540
<212> DNA
<213> Homo sapience

<400> 85

60

tttgaaaaa atg ttg gaa gcc att gac aaa aat cgg gcc ctg cat gca 109

Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

1

5

10

gca gag cgc ttg caa acc aag ctg cga gaa cgt ggg gat gta gca aat 157

Ala Glu Arg Leu Gln Thr Lys Leu Arg Glu Arg Gly Asp Val Ala Asn

15

20

25

gaa gac aaa ctg agc ctt ctg aag tca gtc ctg cag agc cct ctc ttc 205

Glu Asp Lys Leu Ser Leu Leu Lys Ser Val Leu Gln Ser Pro Leu Phe

30

35

40

45

agt cag att ctg agc ctt cag act tct gta cag cag ctg aaa gac cag 253

Ser Gln Ile Leu Ser Leu Gln Thr Ser Val Gln Gln Leu Lys Asp Gln

50

55

60

gta aat att gca act tca gca act tca aat att gaa tat gcc cac gtt 301

Val Asn Ile Ala Thr Ser Ala Thr Ser Asn Ile Glu Tyr Ala His Val

65

70

75

cct cat ctc agc cca gct gtg att cct act ctg caa aat gaa tcg ttt. 349

Pro His Leu Ser Pro Ala Val Ile Pro Thr Leu Gln Asn Glu Ser Phe

80

85

90

tta tta tcc cca aac aat ggg aat ctg gaa gca ctt aca gga cct ggt 397

Leu Leu Ser Pro Asn Asn Gly Asn Leu Glu Ala Leu Thr Gly Pro Gly

00502688-024400

95	100	105	
att cca cac att aat ggg aaa cct gct tgt gat gaa ttt gat cag ctt			445
Ile Pro His Ile Asn Gly Lys Pro Ala Cys Asp Glu Phe Asp Gln Leu			
110	115	120	125
atc aaa aat atg gcc cag ggt cgc cat gta gaa gtt ttt gag ctc ctc			493
Ile Lys Asn Met Ala Gln Gly Arg His Val Glu Val Phe Glu Leu Leu			
	130	135	140
aaa cct cca tct gga ggc ctt ggg ttt agt gtt gtg gga cta aga agt			541
Lys Pro Pro Ser Gly Gly Leu Gly Phe Ser Val Val Gly Leu Arg Ser			
145	150	155	
gaa aac aga gga gag ctg gga ata ttt gtt caa gag ata caa gag ggc			589
Glu Asn Arg Gly Glu Leu Gly Ile Phe Val Gln Glu Ile Gln Glu Gly			
160	165	170	
agt gtg gcc cat aga gat gga aga ttg aaa gaa act gat caa att ctt			637
Ser Val Ala His Arg Asp Gly Arg Leu Lys Glu Thr Asp Gln Ile Leu			
175	180	185	
gct atc aat gga cag gct ctt gat cag aca att aca cat cag cag gct			685
Ala Ile Asn Gly Gln Ala Leu Asp Gln Thr Ile Thr His Gln Gln Ala			
190	195	200	205
atc agc atc ctg cag aaa gcc aaa gat act gtc cag cta gtt att gcc			733

220

235

250

265

285

300

315

320

335

350 355 360 365

370

385

400

415

Ala Val Asp Gly Thr Asn Leu Gln Gly Phe Thr Asn Gln Gln Ala Val

gag gta ttg cga cat aca gga caa act gtg ctc ctg aca cta atg agg 1453

Glu Val Leu Arg His Thr Gly Gln Thr Val Leu Leu Thr Leu Met Arg

450

aga gga atg aag cag gaa gcc gag ctc atg tca agg gaa gac gtc aca 1501

Arg Gly Met Lys Gln Glu Ala Glu Leu Met Ser Arg Glu Asp Val Thr

465

aaa gat gca gat ttg tct cct gtt aat gcc agc ata atc aaa gaa aat 1549

Lys Asp Ala Asp Leu Ser Pro Val Asn Ala Ser Ile Ile Lys Glu Asn

480

tat gaa aaa gat gaa gat ttt tta tct tcg acg aga aac acc aac ata 1597

Tyr Glu Lys Asp Glu Asp Phe Leu Ser Ser Thr Arg Asn Thr Asn Ile

495

tta cca act gaa gaa gaa ggg tat cca tta ctg tca gct gag ata gaa 1645

Leu Pro Thr Glu Glu Glu Gly Tyr Pro Leu Leu Ser Ala Glu Ile Glu

510 515 520 525

gaa ata gaa gat gca caa aaa caa gaa gct gct ctg ctg aca aaa tgg 1693

Glu Ile Glu Asp Ala Gln Lys Gln Glu Ala Ala Leu Leu Thr Lys Trp

Thr Thr Gln Ser Glu Leu Asp Ser Leu Asp Leu Cys Asp Ile Glu Leu

640

645

650

aca gaa aag cct cac gta gat cta ggt gag ttc atc ggg tca tca gag

2077

Thr Glu Lys Pro His Val Asp Leu Gly Glu Phe Ile Gly Ser Ser Glu

655

660

665

cca gag gat cca gtg ctg gcg atg act gat gcg ggt cag agt aca gaa

2125

Pro Glu Asp Pro Val Leu Ala Met Thr Asp Ala Gly Gln Ser Thr Glu

670

675

680

685

gag gtt caa gca cct ttg gcc atg tgg gag gct ggc att cag cac ata

2173

Glu Val Gln Ala Pro Leu Ala Met Trp Glu Ala Gly Ile Gln His Ile

690

695

700

atg ctg gag aaa ggg agc aaa gga ctt ggt ttt agc att tta gat tat

2221

Met Leu Glu Lys Gly Ser Lys Gly Leu Gly Phe Ser Ile Leu Asp Tyr

705

710

715

cag gat cca att gat cca gca agc act gtg att ata att cgt tct ttg

2269

Gln Asp Pro Ile Asp Pro Ala Ser Thr Val Ile Ile Ile Arg Ser Leu

720

725

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gtg cct ggc ggc att gct gaa aag gat gga cga ctt ctt cct ggt gac

2317

Val Pro Gly Gly Ile Ala Glu Lys Asp Gly Arg Leu Leu Pro Gly Asp

735

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745

0050569-04400

cga ctc atg ttt gta aac gat gtt aac ttg gaa aac agc agt ctt gag 2365

Arg Leu Met Phe Val Asn Asp Val Asn Leu Glu Asn Ser Ser Leu Glu

750

755

760

765

gaa gct gta gaa gca ctg aag gga gca ccg tca ggg act gtg aga ata 2413

Glu Ala Val Glu Ala Leu Lys Gly Ala Pro Ser Gly Thr Val Arg Ile

770

775

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gga gtt gct aag cct tta ccc ctt tca cca gaa gaa ggt tat gtt tct 2461

Gly Val Ala Lys Pro Leu Pro Leu Ser Pro Glu Glu Gly Tyr Val Ser

785

790

795

gct aag gag gat tcc ttt ctc tac cca cca cac tcc tgt gag gaa gca 2509

Ala Lys Glu Asp Ser Phe Leu Tyr Pro Pro His Ser Cys Glu Glu Ala

800

805

810

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Gly Leu Ala Asp Lys Pro Leu Phe Arg Ala Asp Leu Ala Leu Val Gly

815

820

825

aca aat gat gct gac tta gta gat gaa tcc aca ttt gag tct cca tac 2605

Thr Asn Asp Ala Asp Leu Val Asp Glu Ser Thr Phe Glu Ser Pro Tyr

830

835

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845

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Ser Pro Glu Asn Asp Ser Ile Tyr Ser Thr Gln Ala Ser Ile Leu Ser

850

855

860

000000-000000

875

890

905

925

940

955

Pro Ser Glu Val Ile Ser Ser Ala Glu Leu Pro Ser Val Leu Pro Asp

960

965

970

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975

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tgt aat gct gag tgt gtc atg ctt caa aat gta tct aaa gaa tct ttt 3085
 Cys Asn Ala Glu Cys Val Met Leu Gln Asn Val Ser Lys Glu Ser Phe

990

995

1000

1005

gaa agg act att aat ata gca aaa ggc aat tct agc cta gga atg aca 3133
 Glu Arg Thr Ile Asn Ile Ala Lys Gly Asn Ser Ser Leu Gly Met Thr

1010

1015

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gtt agt gct aat aaa gat ggc ttg ggg atg atc gtt cga agc att att 3181
 Val Ser Ala Asn Lys Asp Gly Leu Gly Met Ile Val Arg Ser Ile Ile

1025

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atc ttg tcc att aat gaa gag tct acc atc agt gta acc aat gcc cag 3277
 Ile Leu Ser Ile Asn Glu Glu Ser Thr Ile Ser Val Thr Asn Ala Gln

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001120-00000000

1170

1185

1200

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tct gca agc aaa atc tca caa gat gtg gac aaa gag gat gag ttt ggt 3853
Ser Ala Ser Lys Ile Ser Gln Asp Val Asp Lys Glu Asp Glu Phe Gly
1250 1255 1260

ctg cat atg att gaa ctg gag aaa ggt cat agt ggt ttg ggc cta agt 3949
Leu His Met Ile Glu Leu Glu Lys Gly His Ser Gly Leu Gly Leu Ser
1280 1285 1290

ctt gct ggg aac aaa gac cga tcc agg atg agt gtc ttc ata gtg ggg 3997

Leu Ala Gly Asn Lys Asp Arg Ser Arg Met Ser Val Phe Ile Val Gly

1295

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att gat cca aat gga gct gca gga aaa gat ggt cga ttg caa att gca 4045

Ile Asp Pro Asn Gly Ala Ala Gly Lys Asp Gly Arg Leu Gln Ile Ala

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1315

1320

1325

gat gag ctt cta gag atc aat ggt cag att tta tat gga aga agt cat 4093

Asp Glu Leu Leu Glu Ile Asn Gly Gln Ile Leu Tyr Gly Arg Ser His

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cag aat gcc tca tca atc att aaa tgt gcc cct tct aaa gtg aaa ata 4141

Gln Asn Ala Ser Ser Ile Ile Lys Cys Ala Pro Ser Lys Val Lys Ile

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att ttt atc aga aat aaa gat gca gtg aat cag atg gcc gta tgt cct 4189

Ile Phe Ile Arg Asn Lys Asp Ala Val Asn Gln Met Ala Val Cys Pro

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gga aat gca gta gaa cct ttg cct tct aac tca gaa aat ctt caa aat 4237

Gly Asn Ala Val Glu Pro Leu Pro Ser Asn Ser Glu Asn Leu Gln Asn

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1385

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Lys Glu Thr Glu Pro Thr Val Thr Thr Ser Asp Ala Ala Val Asp Leu

001120-0090500

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Ser Ser Phe Lys Asn Val Gln His Leu Glu Leu Pro Lys Asp Gln Gly			
1410	1415	1420	
ggt ttg ggt att gct atc agc gaa gaa gat aca ctc agt gga gtc atc 4381			
Gly Leu Gly Ile Ala Ile Ser Glu Glu Asp Thr Leu Ser Gly Val Ile			
1425	1430	1435	
ata aag agc tta aca gag cat ggg gta gca gcc acg gat gga cga ctc 4429			
Ile Lys Ser Leu Thr Glu His Gly Val Ala Ala Thr Asp Gly Arg Leu			
1440	1445	1450	
aaa gtc gga gat cag ata ctg gct gta gat gat gaa att gtt gtt ggt 4477			
Lys Val Gly Asp Gln Ile Leu Ala Val Asp Asp Glu Ile Val Val Gly			
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tac cct att gaa aag ttt att agc ctt ctg aag aca gca aag atg aca 4525			
Tyr Pro Ile Glu Lys Phe Ile Ser Leu Leu Lys Thr Ala Lys Met Thr			
1470	1475	1480	1485
gta aaa ctt acc atc cat gct gag aat cca gat tcc cag gct gtt cct 4573			
Val Lys Leu Thr Ile His Ala Glu Asn Pro Asp Ser Gln Ala Val Pro			
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Ser Ala Ala Gly Ala Ala Ser Gly Glu Lys Lys Asn Ser Ser Gln Ser

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Leu Met Val Pro Gln Ser Gly Ser Pro Glu Pro Glu Ser Ile Arg Asn

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aca agc aga tca tca aca cca gca att ttt gct tct gat cct gca acc 4717

Thr Ser Arg Ser Ser Thr Pro Ala Ile Phe Ala Ser Asp Pro Ala Thr

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tgc ccc att atc cct ggc tgc gaa aca acc atc gag att tcc aaa ggg 4765

Cys Pro Ile Ile Pro Gly Cys Glu Thr Thr Ile Glu Ile Ser Lys Gly

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1560

1565

cga aca ggg ctg ggc ctg agc atc gtt ggg ggt tca gac acg ctg ctg 4813

Arg Thr Gly Leu Gly Leu Ser Ile Val Gly Gly Ser Asp Thr Leu Leu

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Gly Ala Phe Ile Ile His Glu Val Tyr Glu Glu Gly Ala Ala Cys Lys

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1590

1595

gat gga aga ctc tgg gct gga gat cag atc tta gag gtg aat gga att 4909

Asp Gly Arg Leu Trp Ala Gly Asp Gln Ile Leu Glu Val Asn Gly Ile

1600

1605

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004400-02400

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acg cca cag aga gtg cgc ctg aca ctc tac aga gat gag gcc cca tac 5005
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1635

1640

1645

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1660

ccg gga aaa ggc cta gga tta agt att gtt ggt aaa aga aac gat act 5101
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 Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu Leu Val Asn Gly Glu Asp

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00503699-021100

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His Ser Glu Arg Arg Pro Ser Gln Thr Ser Gln Val Ser Glu Gly Ser

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1755

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Leu Ser Ser Phe Thr Phe Pro Leu Ser Gly Ser Ser Thr Ser Glu Ser

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1765

1770

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Leu Glu Ser Ser Ser Lys Lys Asn Ala Leu Ala Ser Glu Ile Gln Gly

1775

1780

1785

tta aga aca gtc gaa atg aaa aag ggc cct act gac tca ctg gga atc 5485

Leu Arg Thr Val Glu Met Lys Lys Gly Pro Thr Asp Ser Leu Gly Ile

1790

1795

1800

1805

agc atc gct gga gga gta ggc agc cca ctt ggt gat gtg cct ata ttt 5533

Ser Ile Ala Gly Gly Val Gly Ser Pro Leu Gly Asp Val Pro Ile Phe

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Ile Ala Met Met His Pro Thr Gly Val Ala Ala Gln Thr Gln Lys Leu

001120-00000000

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1885

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1935

1945

1950

1955

1960

1965

Gln Ile Ile Ala Val Asn Gly Gln Ser Leu Glu Gly Val Thr His Glu

1970

1975

1980

Glu Ala Val Ala Ile Leu Lys Arg Thr Lys Gly Thr Val Thr Leu Met

1985

1990

1995

Val Leu Ser

2000

cacctcctactgttaaagaga atgcactggt cctgacaatt tttatgctgt gttcagccgg 6170

gtcttcaaaa ctgtaggggg gaaataacac ttaagtttct ttttctcatc tagaaatgct 6230

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<221> CDS

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<400> 86

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tttgaaaaaa atg ttg gaa gcc att gac aaa aat cgg gcc ctg cat gca 109

Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

1

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gca gag cgc ttg caa acc aag ctg cga gaa cgt ggg gat gta gca aat 157

Ala Glu Arg Leu Gln Thr Lys Leu Arg Glu Arg Gly Asp Val Ala Asn

15

20

25

000000-000000

30 35 40 45

50

65 70 75

80 85 90

95 100 105

110 115 120 125

Ile Lys Asn Met Ala Gln Gly Arg His Val Glu Val Phe Glu Leu Leu

140

155

170

185

205

220

235

tct gca gcc agc aca att tca gct cac tct aat ccg gtt cac tgg caa

250

265

285

300

315

330

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acc ctc tcc tca tcc cca act tca acg cca gag ttg cgg gtt gat gct 1165

Thr Leu Ser Ser Ser Pro Thr Ser Thr Pro Glu Leu Arg Val Asp Ala

350 355 360 365

tct act cag aaa ggt gaa gaa agt gag aca ttt gat gta gaa ctc act 1213

Ser Thr Gln Lys Gly Glu Glu Ser Glu Thr Phe Asp Val Glu Leu Thr

370 375 380

aaa aat gtc caa gga tta gga att acc att gct ggc tac att gga gat 1261

Lys Asn Val Gln Gly Leu Gly Ile Thr Ile Ala Gly Tyr Ile Gly Asp

385 390 395

aaa aaa ttg gaa cct tca gga atc ttt gta aag agc att aca aaa agc 1309

Lys Lys Leu Glu Pro Ser Gly Ile Phe Val Lys Ser Ile Thr Lys Ser

400 405 410

agt gcc gtt gag cat gat gga aga atc caa att gga gac caa att ata 1357

Ser Ala Val Glu His Asp Gly Arg Ile Gln Ile Gly Asp Gln Ile Ile

415 420 425

gca gta gat ggc aca aac ctt cag ggt ttt act aat cag caa gca gta 1405

Ala Val Asp Gly Thr Asn Leu Gln Gly Phe Thr Asn Gln Gln Ala Val

430 435 440 445

gag gta ttg cga cat aca gga caa act gtg ctc ctg aca cta atg agg 1453

Glu Val Leu Arg His Thr Gly Gln Thr Val Leu Leu Thr Leu Met Arg

450 455 460

001123-66220560

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Arg Gly Met Lys Gln Glu Ala Glu Leu Met Ser Arg Glu Asp Val Thr

465

470

475

aaa gat gca gat ttg tct cct gtt aat gcc agc ata atc aaa gaa aat 1549

Lys Asp Ala Asp Leu Ser Pro Val Asn Ala Ser Ile Ile Lys Glu Asn

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485

490

tat gaa aaa gat gaa gat ttt tta tct tcg acg aga aac acc aac ata 1597

Tyr Glu Lys Asp Glu Asp Phe Leu Ser Ser Thr Arg Asn Thr Asn Ile

495

500

505

tta cca act gaa gaa gaa ggg tat cca tta ctg tca gct gag ata gaa 1645

Leu Pro Thr Glu Glu Glu Gly Tyr Pro Leu Leu Ser Ala Glu Ile Glu

510

515

520

525

gaa ata gaa gat gca caa aaa caa gaa gct gct ctg ctg aca aaa tgg 1693

Glu Ile Glu Asp Ala Gln Lys Gln Glu Ala Ala Leu Leu Thr Lys Trp

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535

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caa agg att atg gga att aac tat gaa ata gtg gtg gcc cat gtg agc 1741

Gln Arg Ile Met Gly Ile Asn Tyr Glu Ile Val Val Ala His Val Ser

545

550

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aag ttt agt gag aac agt gga ttg ggg ata agc ctg gaa gcg aca gtg 1789

Lys Phe Ser Glu Asn Ser Gly Leu Gly Ile Ser Leu Glu Ala Thr Val

001120-66520560

570

585

605

620

635

650

665

2125

Pro Glu Asp Pro Val Leu Ala Met Thr Asp Ala Gly Gln Ser Thr Glu

670

675

680

685

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2173

Glu Val Gln Ala Pro Leu Ala Met Trp Glu Ala Gly Ile Gln His Ile

690

695

700

atg ctg gag aaa ggg agc aaa gga ctt ggt ttt agc att tta gat tat

2221

Met Leu Glu Lys Gly Ser Lys Gly Leu Gly Phe Ser Ile Leu Asp Tyr

705

710

715

cag gat cca att gat cca gca agc act gtg att ata att cgt tct ttg

2269

Gln Asp Pro Ile Asp Pro Ala Ser Thr Val Ile Ile Ile Arg Ser Leu

720

725

730

gtg cct ggc ggc att gct gaa aag gat gga cga ctt ctt cct ggt gac

2317

Val Pro Gly Gly Ile Ala Glu Lys Asp Gly Arg Leu Leu Pro Gly Asp

735

740

745

cga ctc atg ttt gta aac gat gtt aac ttg gaa aac agc agt ctt gag

2365

Arg Leu Met Phe Val Asn Asp Val Asn Leu Glu Asn Ser Ser Leu Glu

750

755

760

765

gaa gct gta gaa gca ctg aag gga gca ccg tca ggg act gtg aga ata

2413

Glu Ala Val Glu Ala Leu Lys Gly Ala Pro Ser Gly Thr Val Arg Ile

770

775

780

00100-505050

785 790 795

800 805 810

815 820 825

830 835 840 845

850

865

880

Leu Asp Leu His Met Ser Leu Glu Glu Leu Tyr Thr Gln Asn Leu Leu

905

Glu Arg Gln Asp Glu Asn Thr Pro Ser Val Asp Ile Ser Met Gly Pro

925

Ala Ser Gly Phe Thr Ile Asn Asp Tyr Thr Pro Ala Asn Ala Ile Glu

940

Gln Gln Tyr Glu Cys Glu Asn Thr Ile Val Trp Thr Glu Ser His Leu

955

Pro Ser Glu Val Ile Ser Ser Ala Glu Leu Pro Ser Val Leu Pro Asp

970

Ser Ala Gly Lys Gly Ser Glu Tyr Leu Leu Glu Gln Ser Ser Leu Ala

985

Cys Asn Ala Glu Cys Val Met Leu Gln Asn Val Ser Lys Glu Ser Phe

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1010		1015	1020	
gtt agt gct aat aaa gat ggc ttg ggg atg atc gtt cga agc att att				3181
Val Ser Ala Asn Lys Asp Gly Leu Gly Met Ile Val Arg Ser Ile Ile				
1025		1030	1035	
cat gga ggt gcc att agt cga gat ggc cgg att gcc att ggg gac tgc				3229
His Gly Gly Ala Ile Ser Arg Asp Gly Arg Ile Ala Ile Gly Asp Cys				
1040		1045	1050	
atc ttg tcc att aat gaa gag tct acc atc agt gta acc aat gcc cag				3277
Ile Leu Ser Ile Asn Glu Glu Ser Thr Ile Ser Val Thr Asn Ala Gln				
1055		1060	1065	
gca cga gct atg ttg aga aga cat tct ctc att ggc cct gac ata aaa				3325
Ala Arg Ala Met Leu Arg Arg His Ser Leu Ile Gly Pro Asp Ile Lys				
1070		1075	1080	1085
att act tat gtg cct gca gaa cat ttg gaa gag ttc aaa ata agc ttg				3373
Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu				
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gga caa caa tct gga aga gta atg gca ctg gat att ttt tct tca tac				3421

1115

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1145

1165

1180

1195

1210

Met Asp Leu Arg Asp Ala Ser His Glu Gln Ala Val Glu Ala Ile Arg

1225

Lys Ala Gly Asn Pro Val Val Phe Met Val Gln Ser Ile Ile Asn Arg

1245

Pro Arg Lys Ser Pro Leu Pro Ser Leu Leu His Asn Leu Tyr Pro Lys

1260

Tyr Asn Phe Ser Ser Thr Asn Pro Phe Ala Asp Ser Leu Gln Ile Asn

1275

Ala Asp Lys Ala Pro Ser Gln Ser Glu Ser Glu Pro Glu Lys Ala Pro

1290

Leu Cys Ser Val Pro Pro Pro Pro Pro Ser Ala Phe Ala Glu Met Gly

1305

Ser Asp His Thr Gln Ser Ser Ala Ser Lys Ile Ser Gln Asp Val Asp

1325

1340

1355

1370

1385

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1420

Pro Ser Lys Val Lys Ile Ile Phe Ile Arg Asn Lys Asp Ala Val Asn

1435

gat gaa att gtt gtt ggt tac cct att gaa aag ttt att agc ctt ctg 4717

Asp Glu Ile Val Val Gly Tyr Pro Ile Glu Lys Phe Ile Ser Leu Leu

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1540

1545

aag aca gca aag atg aca gta aaa ctt acc atc cat gct gag aat cca

4765

Lys Thr Ala Lys Met Thr Val Lys Leu Thr Ile His Ala Glu Asn Pro

1550

1555

1560

1565

gat tcc cag gct gtt cct tca gca gct ggt gca gcc agt gga gaa aaa

4813

Asp Ser Gln Ala Val Pro Ser Ala Ala Gly Ala Ala Ser Gly Glu Lys

1570

1575

1580

aag aac agc tcc cag tct ctg atg gtc cca cag tct ggc tcc cca gaa

4861

Lys Asn Ser Ser Gln Ser Leu Met Val Pro Gln Ser Gly Ser Pro Glu

1585

1590

1595

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4909

Pro Glu Ser Ile Arg Asn Thr Ser Arg Ser Ser Thr Pro Ala Ile Phe

1600

1605

1610

gct tct gat cct gca acc tgc ccc att atc cct ggc tgc gaa aca acc

4957

Ala Ser Asp Pro Ala Thr Cys Pro Ile Ile Pro Gly Cys Glu Thr Thr

1615

1620

1625

atc gag att tcc aaa ggg cga aca ggg ctg ggc ctg agc atc gtt ggg

5005

Ile Glu Ile Ser Lys Gly Arg Thr Gly Leu Gly Leu Ser Ile Val Gly

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001120-66920550

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1660

gaa gga gca gca tgt aaa gat gga aga ctc tgg gct gga gat cag atc 5101
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1665

1670

1675

tta gag gtg aat gga att gac ttg agg aag gcc aca cat gat gaa gca 5149
 Leu Glu Val Asn Gly Ile Asp Leu Arg Lys Ala Thr His Asp Glu Ala

1680

1685

1690

atc aat gtc ctg aga cag acg cca cag aga gtg cgc ctg aca ctc tac 5197
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1695

1700

1705

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1720

1725

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 Ile Glu Leu Gln Lys Lys Pro Gly Lys Gly Leu Gly Leu Ser Ile Val

1730

1735

1740

ggt aaa aga aac gat act gga gta ttt gtg tca gac att gtc aaa gga 5341
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1745

1750

1755

00502600-021100

1770

1785

1805

1820

1835

1850

Ala Ser Glu Ile Gln Gly Leu Arg Thr Val Glu Met Lys Lys Gly Pro

1865

ggt gat gtg cct ata ttt att gca atg atg cac cca act gga gtt gca 5773
 Gly Asp Val Pro Ile Phe Ile Ala Met Met His Pro Thr Gly Val Ala
 1890 1895 1900

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1905 1910 1915

ggc aca tcc act gag ggc atg act cac acc caa gca gtt aac cta ctg 5869
Gly Thr Ser Thr Glu Gly Met Thr His Thr Gln Ala Val Asn Leu Leu
1920 1925 1930

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Lys Asn Ala Ser Gly Ser Ile Glu Met Gln Val Val Ala Gly Gly Asp
1935 1940 1945

gtg agt gtg gtc aca ggt cat cat cag gag cct gca agt tcc agt ctt	5965
Val Ser Val Val Thr Gly His His Gln Glu Pro Ala Ser Ser Ser Leu	
1950	1955
	1960
	1965

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1980

1995

2010

2025

2045

2060

2070

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25

Glu Asp Lys Leu Ser Leu Leu Lys Ser Val Leu Gln Ser Pro Leu Phe

45

Ser Gln Ile Leu Ser Leu Gln Thr Ser Val Gln Gln Leu Lys Asp Gln

60

Val Asn Ile Ala Thr Ser Ala Thr Ser Asn Ile Glu Tyr Ala His Val

75

Pro His Leu Ser Pro Ala Val Ile Pro Thr Leu Gln Asn Glu Ser Phe

90

Leu Leu Ser Pro Asn Asn Gly Asn Leu Glu Ala Leu Thr Gly Pro Gly

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Ala Arg Ser Ala Ile Glu Glu Arg Thr Ala Pro Thr Ala Leu Gly Ile

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Thr Thr Gln Ser Glu Leu Asp Ser Leu Asp Leu Cys Asp Ile Glu Leu

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Pro Glu Asp Pro Val Leu Ala Met Thr Asp Ala Gly Gln Ser Thr Glu

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735

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745

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770

785

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815

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850

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875

Pro Ser Ser Pro Pro Lys Asp Val Ile Glu Asn Ser Cys Asp Pro Val

890

Leu Asp Leu His Met Ser Leu Glu Glu Leu Tyr Thr Gln Asn Leu Leu

905

Glu Arg Gln Asp Glu Asn Thr Pro Ser Val Asp Ile Ser Met Gly Pro

925

Ala Ser Gly ~~Phe~~ Thr Ile Asn Asp Tyr Thr Pro Ala Asn Ala Ile Glu

940

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955

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